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# OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 80.4786 Seconds

(without alignments) 3085.293 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 571

Sequence: 1.gagctccgagatgaccagtc.....ggaccagctggagatcaaa 321

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-O=/cgn2.1/USPTO\_spool\_p/US09403107/runat\_29082005\_120124\_18882/spp\_query.fasta\_1.1038  
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptc -NORM=ext -HAPSPZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09403107@cgn\_1\_1\_308@runat\_29082005\_120124\_18882 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

1: Geneseq\_16dec04:\*  
2: Geneseqp1980s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	96.1	107	2	AAW80814 Amino aci
2	549	96.1	107	2	AAW17955 Human kap
3	482	84.4	107	2	AAW80817 Amino aci
4	482	84.4	523	3	AAV44994 HD70scFv-
5	482	84.4	523	3	AAV44995 HD70scFv-
6	466	81.6	107	2	AAW54260 Anti-HIV
7	466	81.6	107	2	AAW01283 VL region
8	466	81.6	107	3	AAV98244 Anti-gp12
9	466	81.6	107	3	AAV95135 Anti-gp12
10	465	81.4	107	8	ADP22402 Human ant

11	465	81.4	108	8	ADP47294 Human rho
12	465	81.4	132	2	AAW22842 Human ant
13	464	81.3	107	4	AAW93644 Human ant
14	464	81.3	107	6	ABO27451 Anti-Rh (D
15	464	81.3	108	6	ABP96009 HSA anti-b
16	464	81.3	108	8	ADL92386 Anti-HSA
17	464	81.3	108	8	ADP47113 Human rho
18	464	81.3	108	8	ADQ14601 Single-do
19	464	81.3	108	8	ADQ77191 Dummy VK
20	464	81.3	108	8	ADQ77181 VK dummy
21	464	81.3	108	8	ADQ90912 VK/Ck pro
22	464	81.3	108	8	ADG78333 Vkapra du
23	464	81.3	108	8	ADG78331 Dpkappa9-
24	464	81.3	240	2	AAV02472 A single
25	464	81.3	240	4	AAW46007 Human MUC
26	464	81.3	240	4	AAW46038 Human TF
27	464	81.3	240	4	AAW46008 Human MUC
28	464	81.3	240	4	AAW46006 Human MUC
29	464	81.3	240	4	AAW46005 Human MUC
30	464	81.3	240	6	ABP95997 Human ber
31	464	81.3	240	6	ADL92369 Human pha
32	464	81.3	240	8	ADQ77165 HSA Heavy
33	463	81.1	108	8	ADP47299 Human rho
34	463	81.1	111	4	AAW63656 Amino aci
35	463	81.1	111	6	ABJ38615 Hepaticitis
36	463	81.1	214	8	ADR23360 Human CD7
37	463	81.1	214	8	ADR23358 Human CD7
38	463	81.1	214	8	ADR23366 Human CD7
39	463	81.1	214	8	ADR23364 Human CD7
40	463	81.1	240	6	ABJ38595 Hepaticitis
41	463	81.1	299	4	AAW63660 Amino aci
42	462	80.9	108	6	AAO16706 Human ant
43	462	80.9	240	4	AAW46010 Human MUC
44	462	80.9	245	8	ADR28069 NPb polyP
45	461	80.7	114	2	AAW13922 Light cha

## ALIGNMENTS

RESULT 1	AAW80814	standard; protein; 107 AA.
AC	AAW80814;	
DT	16-FEB-1999	(first entry)
DE	Amino acid sequence of human Kappa 8 light chain variable region.	
XX	Human; kappa 8 light chain variable region; receptor; antigen; tumour;	
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;	
KW	endocrine disease; degenerative disease.	
OS	Homo sapiens.	
XX		
XX	W09846645-A2.	
PD	22-OCT-1998.	
XX		
PF	14-APR-1998;	98WO-EP002180.
XX		
PR	14-APR-1997;	97EP-00106109.
PA	(KUFEE/) KUFER P.	
PA	(RAUM/) RAUM T.	
XX		
PI	Kufer P, Raum T;	
XX		
DR	WPI; 1998-594564/50.	
DR	N-PSDB; AAV68536.	
XX		
PT	Production of anti-human antigen receptors - by selecting a combination of functionally rearranged VH and VL immunoglobulin chains expressed from	

PT a recombinant vector.  
XX  
XX Claim 9; Fig 6; 84pp; English.  
XX  
XX This is the protein sequence of the human kappa 8 light chain variable  
CC region, used in the method of the invention, for providing receptors that  
CC can be used for targeting antigens in humans without being immunogenic  
CC themselves. Such receptors can be used for treating diseases such as  
CC tumours or auto-immune diseases, graft rejection after transplantation,  
CC infectious diseases by targeting cellular receptors as well as allergic,  
CC inflammatory, endocrine and degenerative diseases by targeting key  
CC molecules involved in the pathological process  
XX  
SQ Sequence 107 AA;  
  
Alignment Scores:  
Pred. No.: 1.39e-50 Length: 107  
Score: 549.00 Matches: 105  
Percent Similarity: 98.13% Conservative: 0  
Best Local Similarity: 98.13% Mismatches: 2  
Query Match: 96.15% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-403-107-141 (1-321) x AAW80814 (1-107)  
QY 1 GAGCTCCAGATGACCCGATTCCTCCCTGCTTCTGAGGAGACAGATCACC 60  
DB 1 GlnLeuGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20  
QY 61 ATCACTTGTGGACAAAGTCAGACATTAGCAGCTATTAAATTGGATCAGCAAAACA 120  
DB 21 IleThrCysArgThrSerGlnSerIleSerSerThrLeuAsnTrpYrGlnGlnLysPro 40  
QY 121 GACAGCCTCTTAAGCTGCTCATTTACTGCGCATCTACCCGGGAATCCGGGTCCTGAC 180  
DB 41 GlyGlnProProLysLeuLeuIleYrTrpAlaSerThrArgGlnSerGlyValProAsp 60  
QY 181 CGATTGAGTGGACGGGCTGTCGAGACATTTCATCTCCATCCAGCATCTACCAACT 240  
DB 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
QY 241 GAAGATTCTGCACACTTACTACTGTGACAGAGATTACGACATCCCGTACACTTTGGCCAG 300  
DB 81 GluAspSerAlaThrYrYrCysGlnGlnSerTrpAlaProIleProYrThrPheGlyGln 100  
QY 301 GGGACCAAGCTGGAGATCAAA 321  
DB 101 GlyThrLysLeuGlnIleLys 107  
  
RESULT 2  
AAW17955 ID AAW17955 standard; protein; 107 AA.  
XX  
XX AAW17955;  
XX  
XX 04-AUG-1999 (first entry)  
XX  
XX Human kappa 8 light chain variable region.  
XX  
XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;  
KM autoimmune disease; scFv-antibody; single-chain Fv.  
XX  
XX Homo sapiens.  
XX  
XX WO925818-A1.  
XX  
XX 27-MAY-1999.  
XX  
XX 16-NOV-1998; 98WO-EP007313.  
XX  
XX 17-NOV-1997; 97EP-00120096.  
XX  
XX (KUFE/) KUFER P.

XX  
PI Kufer P, Raum T, Borschert K, Zetcl F, Lutterbuese R;  
XX  
XX WPI; 1999-338004/28.  
DR N-PSDB; AAX77237.  
XX  
XX Phage display system for identification of binding site domains retaining  
PT capacity to bind an epitope.  
XX  
XX Disclosure; Fig 3.2; 152pp; English.  
XX  
XX The invention relates to a method of identifying binding site domains  
CC (BSD) that retain the capacity of binding to a predetermined epitope when  
CC positioned C-terminal of at least one further domain in a recombinant bi-  
CC or multivalent polypeptide. The method comprises (a) testing a panel of  
CC BSD displayed on the surface of a biological display system as part of a  
CC fusion protein for binding to a predetermined epitope, where the fusion  
CC protein comprises an additional domain positioned N-terminal of the BSD  
CC and an amino acid sequence that mediates anchoring of the fusion protein  
CC to the surface of the display system; and (b) identifying a BSD that  
CC binds to the predetermined epitope. The method is useful to identify bi-  
CC or multivalent polypeptides that comprise antibody binding sites capable  
CC of efficiently binding to the corresponding antigen. The polypeptides or  
CC antibodies identified by the method are useful therapeutically and  
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody  
CC fragments that bind independently of their position within bifunctional  
CC single-chain fusion proteins can be isolated from combinatorial antibody  
CC libraries using the new in vitro method  
XX  
SQ Sequence 107 AA;  
  
Alignment Scores:  
Pred. No.: 1.39e-50 Length: 107  
Score: 549.00 Matches: 105  
Percent Similarity: 98.13% Conservative: 0  
Best Local Similarity: 98.13% Mismatches: 2  
Query Match: 96.15% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-403-107-141 (1-321) x AAW17955 (1-107)  
QY 1 GAGCTCCAGATGACCCGATTCCTCCCTGCTTCTGAGGAGACAGATCACC 60  
DB 1 GlnLeuGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20  
QY 61 ATCACTTGTGGACAAAGTCAGACATTAGCAGCTATTAAATTGGATCAGCAAAACA 120  
DB 21 IleThrCysArgThrSerGlnSerIleSerSerThrLeuAsnTrpYrGlnGlnLysPro 40  
QY 121 GACAGCCTCTTAAGCTGCTCATTTACTGCGCATCTACCCGGGAATCCGGGTCCTGAC 180  
DB 41 GlyGlnProProLysLeuLeuIleYrTrpAlaSerThrArgGlnSerGlyValProAsp 60  
QY 181 CGATTGAGTGGACGGGCTGTCGAGACATTTCATCTCCATCCAGCATCTACCAACT 240  
DB 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
QY 241 GAAGATTCTGCACACTTACTACTGTGACAGAGATTACGACATCCCGTACACTTTGGCCAG 300  
DB 81 GluAspSerAlaThrYrYrCysGlnGlnSerTrpAlaProIleProYrThrPheGlyGln 100  
QY 301 GGGACCAAGCTGGAGATCAAA 321  
DB 101 GlyThrLysLeuGlnIleLys 107  
  
RESULT 3  
AAW80817 ID AAW80817 standard; protein; 107 AA.  
XX  
XX AAW80817;  
XX  
XX 16-FEB-1999 (first entry)  
XX

DE	Amino acid sequence of human kappa 5.1 light chain variable region.
KM	Human; kappa 5.1 light chain variable region; receptor; antigen; tumour;
KW	auto-immune disease; graft rejection; allergy; inflammatory disease;
KX	endocrine disease; degenerative disease.
OS	Homo sapiens.
PN	WO9846645-A2.
PD	22-OCT-1998.
XX	
PE	14-APR-1998; 98WO-BP002180.
XX	
PR	14-APR-1997; 97EP-00106109.
XX	
PA	(KUFE/) KUFER P.
XX	(RAUM/) RAUM T.
EI	Kufner P, Raum T;
XX	
DR	WI; 1998-594564/50.
DR	N-PSDB; AAV68539.
XX	
PT	Production of anti-human antigen receptors - by selecting a combination
PT	of functionally rearranged VH and VL immunoglobulin chains expressed from
PT	a recombinant vector.
XX	
PS	Claim 9; Fig 9; 84pp; English.
XX	
CC	This is the amino acid sequence of the human kappa light chain variable
CC	region, used in the method of the invention, for providing receptors that
CC	can be used for targeting antigens in humans without being immunogenic
CC	themselves. Such receptors can be used for treating diseases such as
CC	tumours or auto-immune diseases, graft rejection after transplantation,
CC	infectious diseases by targeting cellular receptors as well as allergic,
CC	inflammatory, endocrine and degenerative diseases by targeting key
CC	molecules involved in the pathological process
SQ	Sequence 107 AA:
Alignment Scores:	
Pred. No.:	2,47e-43 Length: 107
Score:	482.00 Matches: 92
Percent Similarity:	92.52% Conservative: 7
Best Local Similarity:	85.98% Mismatches: 8
Query Match:	84.41% Indels: 0
DB:	Gaps: 0
US-09-403-107-141 (1-321) x AAM80817 (1-107)	
QY	1 GAGGTCGAATGACCGAAGTCTGCATCCTCCGTGCTTCGTTGGGAGACAGAGTCACC 60
Dd	1 GluuuGLInmetrhuInserrProSerSerLeuSerAlaSerValGIyAspATyAlThr 20
QY	61 ATCACTTGTCGACAAGTCAAGACGATTAGACGCTTTAAATTGGTATCAGAGAACA 120
Dd	21 IlleThrCyArgrglAlaserGlInserIlleSerSerTyrlLeuAlentPyTyrgInglInlyPro 40
QY	121 GGAACGCTCTTAAGTGTCTCATTTACTGGCGATTCACCCGGGAATCCGGGGTCCCTGAC 180
Dd	41 GIyGIlnProProLySerLeuLeuIlleTyrlTrpAlaSerThrArgInSerGIyAlProAsp 60
QY	181 CGATTACAGTGGCGGGGTCTGGGACAGATTTCACTCCACATCAGACAGATCTAACCT 240
Dd	61 ArgPheSerGIySerGIuSerGIyThrMetnyTyrlrLeuThrIlleSerSerLeuGIlnPro 80
QY	241 GAAGATTCTGCAACTTACTACTGTGCAGACAGATTACGATCCCGTACACTTTTGGCCAG 300
Dd	81 GIuAsPheAlaleThryrTyrlPheCysGIlnGIlnSerAspSerLeuProIIleThrPheGIyGIln 100
QY	301 GGAGCACAGCTGGAGATCAA 321

Db	101 GlyThyrArgLeuAsp116Gln 107
RESULT 4	
AA44994	
AA44994	standard; protein; 523 AA.
AC	AA44994;
XX	
DT	23-MAY-2000 (first entry)
XX	
DE	HD70scFv-CH1-GM-CSF chain.
XX	
KM	HD70; single-chain variable fragment; scFv; 17-1A antigen; human; BpCAM;
KM	epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
KM	granulocyte/macrophage colony stimulating factor; heteroinibody;
KM	CH1-domain; multifunctional compound; heavy chain constant domain;
KM	immunoglobulin; cytosolic; immunostimulatory; anti-leukaemia; diagnosis;
KM	antiproliferative; prevention; treatment; malignant; haematopoietic cell
KM	lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX	
OS	Homo sapiens.
XX	
PN	WO200006605-A2.
PD	10-FEB-2000.
XX	
PF	28-JUL-1999; 99WO-EP005416.
XX	
PR	28-JUL-1998; 98EP-00114082.
XX	
PA	(MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX	
PI	Kufer P, Dreier T, Baewertle PA, Borschert K, Zetcl F;
XX	
DR	WPI: 2000-195265/17.
DR	N-PSDB; AA250587.
XX	
PT	New multifunctional compounds useful for preventing and/or treating
PT	malignant cell growth and for detection and diagnosis.
XX	
PS	Example 10; Fig 55A; 166pp; English.
XX	
CC	The patent discloses heteroinibodies which are multifunctional compounds
CC	producible in a mammalian host cell as a secretable and fully functional
CC	heterodimer of two polypeptide chains, where one of the polypeptide
CC	chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC	heavy chain) and the other chain comprises CL-domain (constant domain of
CC	an immunoglobulin light chain). The polypeptide chains further comprise,
CC	tuned to the constant domains at least two (polypeptides having
CC	different receptor or ligand functions, where further at least two of the
CC	different (polypeptides) lack an intrinsic affinity for one another and
CC	are linked via the constant domains. The heteroinibodies have
CC	cytotoxic, immunostimulatory, anti-leukaemia and antiproliferative
CC	activities. These compounds can be used for diagnosing, preventing and
CC	treating malignant cell growth related to malignancies of haematopoietic
CC	cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC	melanomas and sarcomas. The present sequence is the left chain of a
CC	heteroinibody comprising HD70 single-chain Fv (scFv) fragment N-
CC	terminally linked to human CH1 domain which bears at its C-terminus the
CC	human inflammatory cytokine granulocyte/macrophage colony stimulating
CC	factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
CC	HD70 scFv specifically recognises the human epithelial cell adhesion
CC	molecule (BpCAM) also called 17-1A antigen
XX	
SO	Sequence 523 AA;
XX	
Alignment Scores:	
Pred. No.:	3,13e-43 Length: 523
Score:	482.00 Matches: 92
Percent Similarity:	92.52% Conservative: 7
Best Local Similarity:	85.96% Mismatches: 8
Query Match:	84.41% Indels: 0
DB:	Gaps: 0

US-09-403-107-141 (1-321) x AAY44995 (1-523)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGCTTCTGTGGAGACAGAGTCACC 60

DB 20 GltLeuGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 39

QY 61 ATCACTTGTCGACAGTTCAGACATTAGACGCTAATTAATGGTATCCAGAAACCA 120

DB 40 IletHrCyArGAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnPro 59

QY 121 GACAGCCTCTTAAGTGTCTATTACTGTGCGATCTAACCCGGGAATCCGGGTCCTGAC 180

DB 60 GlyGlnProProLysLeuLeuIleTyrTrpAlaSerThrArgGlnSerGlyValProAsp 79

QY 181 CGATTACGTGGCAGCGGGTCTGGAGACGATTTCACCTCCATCCAGACTCTACACCT 240

DB 80 ArgPheSerGlySerGlnSerGlyThrAsnTyrThrLeuThrIleSerSerLeuGlnPro 99

QY 241 GAGATTCGTCGAACTTACTACTGTCTGACAGAGATTAGACATCCCGTACCTTTGGCCAG 300

DB 100 GlnAspPheAlaThrTyrPheCysGlnGlnSerAspSerLeuProIleThrPheGlyGln 119

QY 301 GGGACCAAGCTGGAGATCAAA 321

DB 120 GlyThrArgLeuAspIleGln 126

RESULT 5

AAY44995

ID AAY44995 standard; protein; 524 AA.

AC AAY44995;

XX

DT 23-MAY-2000 (first entry)

XX

DE HD70scFv-CK-interleukin 2.

XX

KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human; interleukin-2; CK-domain; kappa light chain constant domain; heteromultimer; multifunctional compound; immunoglobulin; cytostatic; immunostimulatory; antileukemia; diagnosis; prevention; antiproliferative; treatment; malignant; haematopoietic cell; lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.

KW

XX

OS Homo sapiens.

XX

PN WO200006605-A2.

XX

PD 10-FEB-2000.

XX

PF 28-JUL-1999; 99WO-EP005416.

XX

PR 28-JUL-1998; 98EP-00114082.

XX

PA (MICR-) MICROMET GRS BIOMEDIZINISCHE FORSCHUNG.

XX

PI Kufer P, Dreier T, Baeuerle PA, Borechert K, Zettl F;

XX

DR WPI; 2000-195265/17.

DR N-PSDB; AAZ50588.

XX

PT New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis.

XX

PS Example 10; Fig 55B; 166p; English.

XX

CC The patent discloses heteromultimers which are multifunctional compounds producible in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains comprises a CH1-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises a C $\mu$ -domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise,

CC fused to the constant domains at least two (poly)peptides having

CC different receptor or ligand functions, where further at least two of the

CC different (poly)peptides lack an intrinsic affinity for one another and

CC are linked via the constant domains. The heteromultimers have

CC cytostatic, immunostimulatory, antileukemia and antiproliferative

CC activities. These compounds can be used for diagnosing, preventing and

CC treating malignant cell growth related to malignancies of haematopoietic

CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,

CC melanomas and sarcomas. The present sequence is the right chain of a

CC heteromultimer comprising HD70 single-chain Fv (scFv) fragment N-

CC terminally linked to human CK domain (constant domain of immunoglobulin-

CC kappa light chain) which bears at its C-terminus the human inflammatory

CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the

CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen

XX

SO Sequence 524 AA;

Alignment Scores:

Pred. No.: 3,13e-43 Length: 524

Score: 482.00 Matches: 92

Percent Similarity: 92.52% Conservative: 7

Best Local Similarity: 85.98% Mismatches: 8

Query Match: 84,418 Indels: 0

DB: Gaps: 0

US-09-403-107-141 (1-321) x AAY44995 (1-524)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTGCTTCTGTGGAGACAGAGTCACC 60

DB 20 GltLeuGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 39

QY 61 ATCACTTGTCGACAGTTCAGACATTAGACGCTAATTAATGGTATCCAGAAACCA 120

DB 40 IletHrCyArGAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnPro 59

QY 121 GACAGCCTCTTAAGTGTCTATTACTGTGCGATCTAACCCGGGAATCCGGGTCCTGAC 180

DB 60 GlyGlnProProLysLeuLeuIleTyrTrpAlaSerThrArgGlnSerGlyValProAsp 79

QY 181 CGATTACGTGGCAGCGGGTCTGGAGACGATTTCACCTCCATCCAGACTCTACACCT 240

DB 80 ArgPheSerGlySerGlnSerGlyThrAsnTyrThrLeuThrIleSerSerLeuGlnPro 99

QY 241 GAGATTCGTCGAACTTACTACTGTCTGACAGAGATTAGACATCCCGTACCTTTGGCCAG 300

DB 100 GlnAspPheAlaThrTyrPheCysGlnGlnSerAspSerLeuProIleThrPheGlyGln 119

QY 301 GGGACCAAGCTGGAGATCAAA 321

DB 120 GlyThrArgLeuAspIleGln 126

RESULT 6

AAR54260

ID AAR54260 standard; protein; 107 AA.

AC AAR54260;

XX

DT 25-MAR-2003 (revised)

DT 10-NOV-1994 (first entry)

XX

DE Anti-HIV gp120 immunoglobulin light chain variable region b22.

XX

KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope; neutralisation; monoclonal antibody; kappa light chain; variable region; framework; complementarity determining region.

KW

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1..21

FT Region /label= FR1

FT Region 22..33

FT Region /label= CDR1





```
Query Match:      81.61%      Indels:      0
DB:               2          Gaps:          0
US-09-403-107-141 (1-321) x AAM01283 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTCTGCTTGCGGAGACAGAGTCAACCATCACT 66
   1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20
QY 67 TGTGGCAAGTCAAGACATTAGACGCTATTAAATTGTTATCAGCGAACCAGACAG 126
   21 CysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLys 40
QY 127 CCTCCTAAGCTGCTCATTTTACTGCGCATACCCGGGATCCCGGCTGACCGCATTC 186
   41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60
QY 187 AGTGGCAGCGGGTCTGGGACAGATTTCCTCTCAACCATCAGAGTCAACCTGAAGAT 246
   61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 80
QY 247 TCTGCACTTACTACTGTCTGACGACAGATTACGATCCCGTACACTTTTGGCCAGGGGACC 306
   81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGlnGlyThr 100
QY 307 AAGCTGGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

RESULT 8
AAY98244
ID AAY98244 standard; protein; 107 AA.
XX
XX AAY98244;
AC
XX 04-JUL-2000 (first entry)
DT
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
DE
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KM passive immunotherapy; reduce severity; HIV-induced disease;
XX immunocompetence; active immunisation.
XX
XX Homo sapiens.
OS
XX
XX AUY948754-A.
PN
XX
XX 17-FEB-2000.
PD
XX
XX 16-SEP-1999; 99AU-00048754.
PF
XX
XX 16-SEP-1999; 99AU-00048754.
PR
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX
XX Burton DR, Barbas CF, Lerner RA;
PI
XX
XX WPI; 2000-246867/22.
DR
XX
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
PT (HIV) used for providing passive immunotherapy to HIV are specific for
PT glycoprotein-120.
XX
XX Example 9; Fig 11; 374pp; English.
PS
XX
XX This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
CC of reducing an HIV infectivity titre in an in vitro virus infectivity
CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
CC production of the antibody comprises: (a) providing a first
CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
```

```
CC (which does not comprise the sequence represented by AAY98206) and a
CC second polynucleotide encoding a light chain immunoglobulin amino acid
CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of diagnosis and immunotherapy of HIV-induced disease
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
XX
XX SQ Sequence 107 AA;
Alignment Scores:
Pred. No.: 1.33e-41 Length: 107
Score: 466.00 Matches: 90
Percent Similarity: 90.48% Conservative: 5
Best Local Similarity: 85.71% Mismatches: 10
Query Match: 81.61% Indels: 0
DB: 3 Gaps: 0

US-09-403-107-141 (1-321) x AAY98244 (1-107)
QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTCTGCTTGCGGAGACAGAGTCAACCATCACT 66
   1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20
QY 67 TGTGGCAAGTCAAGACATTAGACGCTATTAAATTGTTATCAGCGAACCAGACAG 126
   21 CysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLys 40
QY 127 CCTCCTAAGCTGCTCATTTTACTGCGCATACCCGGGATCCCGGCTGACCGCATTC 186
   41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60
QY 187 AGTGGCAGCGGGTCTGGGACAGATTTCCTCTCAACCATCAGAGTCAACCTGAAGAT 246
   61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 80
QY 247 TCTGCACTTACTACTGTCTGACGACAGATTACGATCCCGTACACTTTTGGCCAGGGGACC 306
   81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGlnGlyThr 100
QY 307 AAGCTGGAGATCAAA 321
Db 101 LysLeuGlnIleLys 105

RESULT 9
AAY95135
ID AAY95135 standard; protein; 107 AA.
XX
XX AAY95135;
AC
XX
XX 30-JUN-2000 (first entry)
DT
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
DE
XX
XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
```





DT		12-SEP-1997	(first entry)
XX			
DE			Human anti-tumour antigen antibody light chain variable region.
XX			
KW			Human; tumour antigen; cancer; monoclonal; antibody; light chain;
KW			variable region; medicine; pharmacology; biochemistry; CDR;
KW			complementarity determining region.
XX			
OS			Homo sapiens.
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..22	
FT		/label= sig_peptide	
FT	Peptide	23..132	
FT		/label= mat_peptide	
FT	Region	46..56	
FT		/label= CDR_1	
FT	Region	72..78	
FT		/label= CDR_2	
FT	Region	111..119	
FT		/label= CDR_3	
XX			
PN			JP09100300-A.
XX			
PD	15-APR-1997.		
XX			
PP	03-OCT-1995;	95UP-00278266.	
XX			
PR	03-OCT-1995;	95UP-00278266.	
XX			
PA	(HAGI/) HAGIMARA Y.		
XX			
DR	WPI; 1997-276726/25.		
DR	N-PSDB; AAT75423.		
PT			
XX			
PT	Anticancer human monoclonal antibody variable region sequences - and related DNA and RNA.		
XX			
PS	Claim 9; Page 11; 14pp; Japanese.		
CC			
CC	The present sequence is a human anti-tumour antigen monoclonal antibody (Mab) light chain variable region, useful in medicine, pharmacology and biochemistry. The isotype of a Mab secreted by the human/human hybridoma HT was determined to be mu and kappa. Human Mab was purified, and the antigen recognised by human Mab CLN"-IgM identified by western blotting		
CC			
SO	Sequence 132 AA;		
	Alignment Scores:		
OY	Pred. No.: 1.76e-41	Length: 132	
	Score: 465.00	Matches: 90	
Db	Percent Similarity: 89.72%	Conservative: 6	
	Best Local Similarity: 84.11%	Mismatches: 11	
	Query Match: 81.44%	Indels: 0	
Db:	2	Gaps: 0	
US-09-403-107-141	(1-321) x AAM22842 (1-132)		
OY	1 GAGCTTCACGATGATACCAGTCTCATCTCCTCGTGCTTGTGGAGACAGAGTCACC	60	
	.....		
Db	23 AAGTTGImetThrcInserProSerSerLeuSerAlaSerValAllyspArGValThr	42	
OY	61 ATCACTTGCGGACAAGTCAGAGCATTAACAGCTATTAAATTGATATCAGCAAGAACC	120	
Db	43 IlenrCyBaXAlaSerGlnSerIleSerSerTyLeuAsnTrpYrgInGlnLysPro	62	
OY	121 GGACAGCCTCTTAGCTGCTCATTTACTGGCGATCTACCGGGGAATCCGGGGTCCCTGAC	180	
Db	63 GlyValaIaProLyLeuLeuIeTyAlaIaLaSerSerLeuGlnSerGlyValProSer	82	
OY	181 CGATTTCAGTGGCAGCGGGGTCTGGAGACAGATTTACTCTCACCATCAGCAAGTCAACCT	240	
Db	83 ArGPlaeSeGlySerIySerGlyThrApPheThrLeuThrIleSerSerLeuGlnPro	1020	

```
QY      2A1 |AAAGTTCTGCACACTTACTACTGTGAGAGAATTCAGCATCCCGCACTTTTGCCGAG 308
Db      103 |GUAAPePhealathrTyTrtytgcgInglngInsertRyserThProGlntHrPhneIygin 122
QY      301 GGGACCACAGCTGAGATCAA 321
Db      123 |GlyThrLyValGIuilellys 129

RESULT 13
ID      AAG93644 standard; protein; 107 AA.
XX      AC      AAG93644;
DT      DT      14-SEP-2001 (first entry)
DE      DE      Human anti-Rh(D) antibody clone SH13 protein sequence.
XX      XX      Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW      KW      red blood cell; Rh phenotype; diagnosis; therapeutic.
OS      OS      Homo sapiens.
PN      PN      US6255455-B1.
PD      PD      03-JUL--2001.
PF      PF      29-JAN-1999;    99US-00240274.
PR      PR      11-OCT-1996;    96US-0028550P.
PR      PR      27-JUN-1997;    97US-0088404S.
PR      PR      10-APR-1998;    98US-0081380P.
PA      PA      (TYPE-) UNIV PENNSYLVANIA.
PI      PI      Siegel DL;
XX      XX      WPT: 2001-388931/41.
DR      DR      N-PESDB; AAH68701.
PT      PT      New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT      PT      diagnostics requiring a human instead of an animal antibody and in
XX      XX      therapeutic medicine.
PS      PS      Claim 1; Col 68; 162pp; English.
CC      CC      The present invention describes an isolated Rh(D) binding protein,
CC      CC      preferably a human antibody, (I) having an amino acid sequence comprising
CC      CC      one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC      CC      immunostimulant activity, and can be used as an immune system stimulant.
CC      CC      (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC      CC      are used in diagnostics that require human antibodies instead of animal
CC      CC      antibodies, such as determine the Rh phenotype of human red blood cells.
CC      CC      AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC      CC      AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC      CC      chain CDR3 amino acid sequences which are given in the exemplification of
XX      XX      the present invention
SQ      SQ      Sequence 107 AA;

Alignment Scores:
Pred.No.:          2,198-41         Length:           107
Score:             464.00            Matches:           90
Percent Similarity: 89.52%           Conservative:       4
Best Local Similarity: 85.71%        Mismatches:        11
Query Match:       81.26%            Indels:            0
DB:                4                 Gaps:              0

US-09-403-107-141 (1-321) x AAG93644 (1-107)
```

```

Db      2  GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 21
QY      67  TGTGGCAAGTCAAGCATTTAGCAGCTATTAAATTGGTATCAAGCAAAACAGAGACAG 126
Db      22  CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnLysProGlyLys 41
QY      127  CCTCCCTAAGCTGCTATTACTGCGGATCCGCGGATCCGCGGATCCCTGACCGATTG 186
Db      42  AlaProlyLeuLeuIleTyAlaAlaSerSerLeuArgSerGlyValProSerArgPhe 61
QY      187  AGTGGCAGCGGGTCTGGGACAGATTTCACCTCAGCAGTCAAGCTTACAACTGAAGAT 246
Db      62  SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 81
QY      247  TCTGCACACTTACTACTGTGCGAGAGATTACAGACATCCCGTACACTTTGGCCAGGGACC 306
Db      82  PheAlaThrTyTrpCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 101
QY      307  AAGCTGGAGATCAAA 321
Db      102  LysLeuGlnIleLys 106

```

RESULT 14  
ID ABO27451 standard; protein; 107 AA.

AC ABO27451;

DT 12-SEP-2003 (first entry)

DE Anti-Rh(D) light chain SH13.

KM Human; RH(D) binding protein; blood typing; blood product; antibody;

XX magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2003-512273/48.

XX N-PSDB; ACD45365.

XX New human Rh(D)-binding protein useful for various diagnostic and

PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 50; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein

CC can be used for magnetically activated cell sorting. The protein is

CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence

CC represents the amino acid sequence of a human anti-Rh(D) chain

XX

SQ Sequence 107 AA;

Alignment Scores:

Pred. No.: 2.19e-41

Score: 464.00

Percent Similarity: 89.52%

Best Local Similarity: 85.71%

Query Match: 81.26% Indels: 0

DB: 6 Gaps: 0

US-09-403-107-141 (1-321) x ABO27451 (1-107)

```

QY      7  CAGATGACCAGTCTCCATCTCCCTGCTGCTTGTGGAGACAGACTCACTACT 66
Db      2  GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 21
QY      67  TGTGGCAAGTCAAGCATTTAGCAGCTATTAAATTGGTATCAAGCAAAACAGAGACAG 126
Db      22  CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnLysProGlyLys 41
QY      127  CCTCCCTAAGCTGCTATTACTGCGGATCCGCGGATCCGCGGATCCCTGACCGATTG 186
Db      42  AlaProlyLeuLeuIleTyAlaAlaSerSerLeuArgSerGlyValProSerArgPhe 61
QY      187  AGTGGCAGCGGGTCTGGGACAGATTTCACCTCAGCAGTCAAGCTTACAACTGAAGAT 246
Db      62  SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 81
QY      247  TCTGCACACTTACTACTGTGCGAGAGATTACAGACATCCCGTACACTTTGGCCAGGGACC 306
Db      82  PheAlaThrTyTrpCysGlnGlnSerTySerThrProTyThrPheGlyGlnGlyThr 101
QY      307  AAGCTGGAGATCAAA 321
Db      102  LysLeuGlnIleLys 106

```

RESULT 15

ID ABP96009 standard; protein; 108 AA.

AC ABP96009;

DT 01-MAY-2003 (first entry)

DE HSA antibody related Vkappa chain Vkappa dummy.

XX

XX Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV;

XX anti-inflammatory; antianemic; immunosuppressive; neuroprotective;

XX dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia;

XX inflammation; autoimmune disorder; multiple sclerosis; Crohn's disease;

XX myasthenia gravis.

XX Homo sapiens.

OS Synthetic.

PN WO2003002609-A2.

XX 09-JAN-2003.

XX 28-JUN-2002; 2002WO-GB003014.

XX 28-JUN-2001; 2001GB-00015841.

XX (MEDT-) MEDICAL RES COUNCIL.

XX Winter G; Ignatovich O; Tomlinson I;

XX WPI; 2003-210246/20.

XX Dual-specific ligand having immunoglobulins with binding specificity to

PT different antigens or epitopes, useful for treating, preventing or

PT diagnosing diseases, e.g. cancer, HIV infection, inflammations, or

PT myasthenia gravis.

XX Example 1; Fig 3; 84pp; English.

XX The present invention describes a dual-specific ligand (I) comprising:

CC (a) a first single immunoglobulin variable domain with a binding

CC specificity to a first antigen or epitope; and (b) a second complementary

CC immunoglobulin single variable domain with a binding activity to a second

CC antigen or epitope. The binding domains are mutually complementary, and  
CC the first and second domains lack mutually complementary domains that  
CC share the same specificity. (1) has cytostatic, anti-HIV, antianaemic,  
CC antiinflammatory, immunosuppressive and neuroprotective activities. The  
CC dual-specific ligand is useful for treating, preventing or diagnosing  
CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,  
CC inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's  
CC disease or myasthenia gravis). The dual-specific ligand may be used to  
CC recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is  
CC also useful for monitoring the efficacy of drugs, as well as for  
CC monitoring toxicity. The present sequence represents a human serum  
CC albumin (HSA) related antibody Vkapra sequence, which is used in an  
CC example from the present invention

XX Sequence 108 AA;

Alignment Scores:

Pred. No.:	2,19e-41	Length:	108
Score:	464.00	Matches:	90
Percent Similarity:	89.72%	Conservative:	6
Best Local Similarity:	84.11%	Mismatches:	11
Query Match:	81.26%	Indels:	0
DB:	6	Gaps:	0

US-09-403-107-141 (1-321) x ABP96009 (1-108)

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QY      1 GAGCTCCGAGATGACCCAGTTCCTCCCTGCTGCTGCGGAGACAGATCAC 60
        : : : : :
Db      1 AspliegImetThGInSerProSerSerLeuSerValGlyAspArgValThr 20

QY      61 ATCACTTGCGAGACAAGTCAGAGCATTTAGCAGCTATTAATGGTATCAGAGAAACA 120
        : : : : :
Db      21 IleThrCysArgAlaSerGlnSerIleSerSerThrLeuAsnTrpTyrGlnGlnPro 40

QY      121 GGACAGCCTCTTAAGCTCTCATTTACTGCGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
        : : : : :
Db      41 GlyysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60

QY      181 CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTCACCTCACCATCAGCAGTCTACAACCT 240
        : : : : :
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80

QY      241 GAAGATTCGCAACTTACTACTGTCAGCAGAGATTACGATCCGGTACACTTTGGCCAG 300
        : : : : :
Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProAsnThrPheGlyGln 100

QY      301 GGGACCAAGCTGAGATCAAA 321
        : : : : :
Db      101 GlyThrLysValGlnIleLys 107
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Job time : 84.4786 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_nzp model

Run on: August 29, 2005, 11:01:36 ; Search time 17.1474 Seconds  
(without alignments)  
2794.861 Million cell updates/sec

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Perfect score: 571  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
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Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 1027090

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Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	81.6	107	1	US-08-276-852-104 Sequence 104, App
2	466	81.6	107	1	US-08-899-575-104 Sequence 104, App
3	466	81.6	107	1	US-08-899-575-104 Sequence 104, App
4	466	81.6	107	5	PCT-US95-08743-104 Sequence 104, App
5	464	81.3	107	3	US-09-240-274-156 Sequence 156, App
6	464	81.3	240	4	US-09-192-854-2 Sequence 2, Appli
7	463	81.1	109	3	US-09-157-370-3 Sequence 105, App
8	458	80.2	107	1	US-08-276-852-105 Sequence 105, App
9	458	80.2	107	1	US-08-899-575-105 Sequence 105, App
10	458	80.2	107	1	US-08-899-575-105 Sequence 105, App
11	458	80.2	107	5	PCT-US95-08743-105 Sequence 105, App
12	458	80.2	108	2	US-08-379-057-29 Sequence 29, Appl

13	457	80.0	107	3	US-09-240-274-175 Sequence 175, App
14	457	80.0	107	3	US-09-240-274-176 Sequence 176, App
15	455.5	79.8	108	3	US-09-240-274-32 Sequence 32, Appl
16	455.5	79.8	108	3	US-09-240-274-43 Sequence 43, Appl
17	455	79.7	107	3	US-09-240-274-37 Sequence 37, Appl
18	455	79.7	111	1	US-08-137-117D-67 Sequence 67, Appl
19	455	79.7	111	2	US-08-436-717-67 Sequence 67, Appl
20	455	79.7	126	1	US-08-137-117D-71 Sequence 71, Appl
21	455	79.7	126	2	US-08-436-717-71 Sequence 71, Appl
22	452.5	79.2	108	3	US-09-240-274-167 Sequence 167, App
23	452	79.2	127	3	US-08-836-561-71 Sequence 71, Appl
24	452	79.2	127	4	US-09-434-122-71 Sequence 71, Appl
25	452	79.2	134	3	US-08-718-323A-10 Sequence 10, Appl
26	452	79.2	134	4	US-09-587-526-10 Sequence 10, Appl
27	451	79.0	109	3	US-07-934-373C-3 Sequence 3, Appli
28	451	79.0	109	3	US-07-934-373C-3 Sequence 3, Appli
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30	451	79.0	109	4	US-08-146-206C-3 Sequence 3, Appli
31	451	79.0	109	4	US-09-705-686-3 Sequence 3, Appli
32	451	79.0	109	4	US-09-705-392A-3 Sequence 3, Appli
33	451	79.0	109	5	PCT-US93-07832-33 Sequence 3, Appli
34	451	79.0	127	3	US-08-284-516C-57 Sequence 57, Appl
35	451	79.0	127	4	US-09-537-911A-57 Sequence 57, Appl
36	451	79.0	214	2	US-07-934-373C-39 Sequence 39, Appl
37	451	79.0	214	2	US-08-437-642B-39 Sequence 39, Appl
38	451	79.0	214	5	PCT-US93-07832-39 Sequence 39, Appl
39	450	78.8	104	1	US-08-276-852-106 Sequence 106, App
40	450	78.8	104	1	US-08-899-575-106 Sequence 106, App
41	450	78.8	104	1	US-08-899-575-106 Sequence 106, App
42	450	78.8	104	5	PCT-US95-08743-106 Sequence 106, App
43	450	78.8	107	2	US-08-652-558-36 Sequence 36, Appl
44	450	78.8	107	2	US-08-378-939-14 Sequence 14, Appl
45	449	78.6	107	3	US-09-240-274-179 Sequence 179, App

## ALIGNMENTS

RESULT 1  
US-08-276-852-104  
Sequence 104, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-104

Alignment Scores:  
Pred. No.: 6.3e-49 Length: 107  
Score: 466.00 Matches: 90  
Percent Similarity: 90.48% Conservative: 5  
Best Local Similarity: 85.71% Mismatches: 10  
Query Match: 81.61% Indels: 0  
DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x US-08-276-852-104 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTTGTGGGAGACAGATCAACATCACT 66  
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCAAGACATTAGACGCTATTAAATTGGTATGACGAAACAGACAG 126  
Db 21 CysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnIlypProGlyLys 40

QY 127 CCTCCTAAGCTGCTCACTTCTGCGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTG 186  
Db 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerIlyValProSerArgPhe 60

QY 187 AGTGGACGGGCTCTGGGACAGATTTCACCTCAGCATCAGACGATCAACCTGAAGAT 246  
Db 61 SerGlySerIlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyAsp 80

QY 247 TGTGGCAACTTACTGTGTCAGACAGATTAGACATCCGTCACCTTTGGCCAGGGACC 306  
Db 81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGlnIlyThr 100

QY 307 AAGCTGAGATCAAA 321  
Db 101 LysLeuGlnIlyLeys 105

RESULT 2  
US-08-899-575-104  
Sequence 104, Application US/08899575  
Patent No. 5770440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-104

Alignment Scores:  
Pred. No.: 6.3e-49 Length: 107  
Score: 466.00 Matches: 90  
Percent Similarity: 90.48% Conservative: 5  
Best Local Similarity: 85.71% Mismatches: 10  
Query Match: 81.61% Indels: 0  
DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x US-08-899-575-104 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTTGTGGGAGACAGATCAACATCACT 66  
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGCAAGTCAAGACATTAGACGCTATTAAATTGGTATGACGAAACAGACAG 126  
Db 21 CysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnIlypProGlyLys 40

QY 127 CCTCCTAAGCTGCTCACTTCTGCGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTG 186  
Db 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGGACGGGCTCTGGGACAGATTTCACCTCAGCATCAGACGATCAACCTGAAGAT 246  
Db 61 SerGlySerIlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyAsp 80

QY 247 TGTGGCAACTTACTGTGTCAGACAGATTAGACATCCGTCACCTTTGGCCAGGGACC 306  
Db 81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProTyrThrPheGlyGlnIlyThr 100

QY 307 AAGCTGAGATCAAA 321  
Db 101 LysLeuGlnIlyLeys 105

RESULT 3  
US-08-899-575-104  
Sequence 104, Application US/08899575  
Patent No. 5804440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of  
 ADDRESSEE: Patent Counsel  
 STREET: 10666 NO. 58044th Torrey Pines Road, Suite 220,  
 STREET: Mail Drop 1PC8  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/899,575  
 FILING DATE: 24-JUL-1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/276,852  
 FILING DATE: 18-JUL-1994  
 APPLICATION NUMBER: US 08/178,302  
 FILING DATE: 30-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/954,148  
 FILING DATE: 30-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: SCR1452P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 104:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-899-575-104  
 Alignment Scores:  
 Pred. No.: 6.3e-49 Length: 107  
 Score: 466.00 Matches: 90  
 Percent Similarity: 90.48% Conservative: 5  
 Best Local Similarity: 85.71% Mismatches: 10  
 Query Match: 81.61% Indels: 0  
 Gaps: 0  
 US-09-403-107-141 (1-321) x US-08-899-575-104 (1-107)  
 QY 7 CAGATGACCCAGTCTCCATCTCTGCTTGTGGAGACAGATCACCATCACT 66  
 Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20  
 QY 67 TGTGGCAAGTCAGACGATTAGCAGCTATTAAATTGATATCGACAGAAACGAGAC 126  
 Db 21 CysArgAlaSerGlnSerIleSerSerIleuSerThrIleuSerLeuGlnLysProGlnLys 40  
 QY 127 CCTCTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 186  
 Db 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60  
 QY 187 AGTGGACGGGGTCTGGAGACGATTTCATCTCACCATCAGACGCTTCAACCTGAAGAT 246  
 Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnLys 80  
 QY 247 TCTGCACTTACTACTGTCAGACAGATTAGACATCCGTCACATTTGGCCAGGGAGCC 306  
 Db 81 PheAlaThrTyrTyrCysGlnGlnSerIleSerThrProTyrThrPheGlyGlnGlyThr 100  
 QY 307 AAGCTGAGATCAAA 321  
 Db 101 LysLeuGlnIleLys 105

RESULT 4  
 PCT-US95-08743-104  
 Sequence 104, Application PC/TUS9508743  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 NUMBER OF SEQUENCES: 170  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25 (ERO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/08743  
 FILING DATE: 11-JUL-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/276,852  
 FILING DATE: 18-JUL-1994  
 INFORMATION FOR SEQ ID NO: 104:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-08743-104  
 Alignment Scores:  
 Pred. No.: 6.3e-49 Length: 107  
 Score: 466.00 Matches: 90  
 Percent Similarity: 90.48% Conservative: 5  
 Best Local Similarity: 85.71% Mismatches: 10  
 Query Match: 81.61% Indels: 0  
 Gaps: 0  
 US-09-403-107-141 (1-321) x PCT-US95-08743-104 (1-107)  
 QY 7 CAGATGACCCAGTCTCCATCTCTGCTTGTGGAGACAGATCACCATCACT 66  
 Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20  
 QY 67 TGTGGCAAGTCAGACGATTAGCAGCTATTAAATTGATATCGACAGAAACGAGAC 126  
 Db 21 CysArgAlaSerGlnSerIleSerSerIleuSerThrIleuSerLeuGlnLysProGlnLys 40  
 QY 127 CCTCTAAGCTGCTCATTACTGCGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 186  
 Db 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60  
 QY 187 AGTGGACGGGGTCTGGAGACGATTTCATCTCACCATCAGACGCTTCAACCTGAAGAT 246  
 Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnLys 80  
 QY 247 TCTGCACTTACTACTGTCAGACAGATTAGACATCCGTCACATTTGGCCAGGGAGCC 306  
 Db 81 PheAlaThrTyrTyrCysGlnGlnSerIleSerThrProTyrThrPheGlyGlnGlyThr 100  
 QY 307 AAGCTGAGATCAAA 321  
 Db 101 LysLeuGlnIleLys 105  
 RESULT 5  
 US-09-240-274-156  
 Sequence 156, Application US/09240274  
 Patent No. 6255455  
 GENERAL INFORMATION:  
 APPLICANT: Siegel, Donald L.  
 TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 FILE REFERENCE: 09596-4202  
 CURRENT APPLICATION NUMBER: US/09/240,274  
 CURRENT FILING DATE: 1999-01-29



QY 121 GGACAGCCTCTAGCTGCTATTCTAGTCGACATCCCGGAGATCCGGGCTCCCTGAC 180  
 Db 41 GILYLSALAEPROLYSEULEULETYRPAALASERALEUGHSERGLYVALPROSER 60  
 QY 181 CGATTTCAGTGGAGCGGCTGCGACAGATTTCACCTTCACCATCAGCAGTTCAGACT 240  
 Db 61 ArgpneserGlySerGlySerGlyThrAspPheThrIleSerSerLeuGlnPro 80  
 QY 241 GAGATTCTGCACTTACTCTGTCAGCAGAGTTACGACATCCCGTACCTTTGGCGAG 300  
 Db 81 GluaepPhealaThrTyrrCySGInGlnIrrTyrrSerLeuProTyrrPheGlyGln 100  
 QY 301 GGGACCAAGCTGAGATCAAA 321  
 Db 101 GILYrLYSVALGILUILEYS 107  
 RESULT 8  
 US-08-276-852-105  
 ; Sequence 105, Application US/08276852  
 ; Patent No. 5652138  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burton, Dennis R  
 ; APPLICANT: Barbos, Carlos F  
 ; APPLICANT: Lerner, Richard A  
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 ; NUMBER OF SEQUENCES: 170  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: The Scripps Research Institute, Office of  
 ; ADDRESSEE: Patent Counsel  
 ; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
 ; STREET: Mail Drop TPC8  
 ; CITY: La Jolla  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/276,852  
 ; FILING DATE: 18-JUL-1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/178,302  
 ; FILING DATE: 30-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/954,148  
 ; FILING DATE: 30-SEP-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fitting, Thomas  
 ; REGISTRATION NUMBER: 34,163  
 ; REFERENCE/DOCKET NUMBER: SCR1452P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-554-2937  
 ; TELEFAX: 619-554-6312  
 ; INFORMATION FOR SEQ ID NO: 105:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 107 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-276-852-105  
 Alignment Scores:  
 Pred. No.: 6 098-48 Length: 107  
 Score: 458.00 Matches: 89  
 Percent Similarity: 89.52% Conservative: 5  
 Best Local Similarity: 84.76% Mismatches: 11  
 Query Match: 80.21% Indels: 0  
 DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x US-08-276-852-105 (1-107)  
 QY 7 CAGATGACCCAGTCTCATCTCCCTGCTTCTGTGGAGACAGAGTGCATCATCT 66  
 Db 1 GlueuthrGlnSerProSerSerLeuSerSerValGlyAspArgValThrIleThr 20  
 QY 67 TGTGGACAGTCTCAGCAGATTAGCAGATTAAATTGTTTCAGCAGAAACCGAGACG 126  
 Db 21 CysArgAlaSerGlnSerIleSerSerTyrrLeuSerThrProGlnGlnLysProGlyLys 40  
 QY 127 CTTCTAAGCTGCTCATTTACTGCGAGATCCCGGAGATCCGGGCTCCCTGACCGATTTC 186  
 Db 41 AlaProLysLeuLeuIleTyrrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60  
 QY 187 AGTGCAGCGGCTGCGACAGATTTCATCTCAGCATCAGCAGTTCAGTTCAGAT 246  
 Db 61 SerGlySerGlySerGlyThrAspPheThrIleSerSerLeuGlnProGlnLysp 80  
 QY 247 TCTGCACTTACTCTGTCAGCAGAGTTACGACATCCCGTACCTTTGGCCAGGGAGCC 306  
 Db 81 PhealaThrTyrrCySGInGlnSerTyrrSerThrProGlnThrPheGlyGlnGlyThr 100  
 QY 307 AAGCTGAGATCAAA 321  
 Db 101 LysLeuGlnIleLys 105  
 RESULT 9  
 US-08-899-575-105  
 ; Sequence 105, Application US/08899575  
 ; Patent No. 5770440  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burton, Dennis R  
 ; APPLICANT: Barbos, Carlos F  
 ; APPLICANT: Lerner, Richard A  
 ; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
 ; NUMBER OF SEQUENCES: 170  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: The Scripps Research Institute, Office of  
 ; ADDRESSEE: Patent Counsel  
 ; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
 ; STREET: Mail Drop TPC8  
 ; CITY: La Jolla  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/899,575  
 ; FILING DATE: 24-JUL-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/276,852  
 ; FILING DATE: 18-JUL-1994  
 ; APPLICATION NUMBER: US 08/178,302  
 ; FILING DATE: 30-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/954,148  
 ; FILING DATE: 30-SEP-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fitting, Thomas  
 ; REGISTRATION NUMBER: 34,163  
 ; REFERENCE/DOCKET NUMBER: SCR1452P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-554-2937  
 ; TELEFAX: 619-554-6312  
 ; INFORMATION FOR SEQ ID NO: 105:  
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Alignment Scores:  
Pred. No.: 6 09e-48 Length: 107  
Score: 458.00 Matches: 89  
Percent Similarity: 89.52% Conservative: 5  
Best Local Similarity: 84.76% Mismatches: 11  
Query Match: 80.21% Indels: 0  
Gaps: 0

US-09-403-107-141 (1-321) x US-08-899-575-105 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTTGTGTGGAGACAGAGTCAACCTACT 66  
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGCGACAAGTCAGACGATTAGCAGCTATTAATGGTATACAGCAGAAACGAGACAG 126  
Db 21 CysArgAlaSerGlnSerIleSerSerIleuAsnTrpGlnGlnLysProGlyLys 40

QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATACCCGGGAATCCGGGGTCCCTGACCGATTG 186  
Db 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGGACGGGGTCTGGGACAGATTTCACCTTCACATCAGAGTCTACAACTGAAGAT 246  
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 80

QY 247 TGTGCAACTTACTCTGTCAGACAGATTAGACATCCCGTCACTTTGGCCAGGGGACC 306  
Db 81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProGlnThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321  
Db 101 LysLeuGlnIleLys 105

RESULT 10  
US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5804440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbias, Carlos F  
TITLE OF INVENTION: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302

FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRL452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Alignment Scores:  
Pred. No.: 6 09e-48 Length: 107  
Score: 458.00 Matches: 89  
Percent Similarity: 89.52% Conservative: 5  
Best Local Similarity: 84.76% Mismatches: 11  
Query Match: 80.21% Indels: 0  
Gaps: 0

US-09-403-107-141 (1-321) x US-08-899-575-105 (1-107)

QY 7 CAGATGACCCAGTCTCCATCTCCCTGCTTGTGTGGAGACAGAGTCAACCTACT 66  
Db 1 GluLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThr 20

QY 67 TGTGCGACAAGTCAGACGATTAGCAGCTATTAATGGTATACAGCAGAAACGAGACAG 126  
Db 21 CysArgAlaSerGlnSerIleSerSerIleuAsnTrpGlnGlnLysProGlyLys 40

QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATACCCGGGAATCCGGGGTCCCTGACCGATTG 186  
Db 41 AlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 60

QY 187 AGTGGACGGGGTCTGGGACAGATTTCACCTTCACATCAGAGTCTACAACTGAAGAT 246  
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAsp 80

QY 247 TGTGCAACTTACTCTGTCAGACAGATTAGACATCCCGTCACTTTGGCCAGGGGACC 306  
Db 81 PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProGlnThrPheGlyGlnGlyThr 100

QY 307 AAGCTGAGATCAAA 321  
Db 101 LysLeuGlnIleLys 105

RESULT 11  
PCT-US95-08743-105  
Sequence 105, Application PC/TUS9508743  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08743  
FILING DATE: 11-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08743-105

Alignment Scores:  
Pred. No.: 6,09e-48 Length: 107  
Score: 458.00 Matches: 89  
Percent Similarity: 89.52% Conservative: 5  
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Query Match: 80.21% Indels: 0  
DB: 5 Gaps: 0

US-09-403-107-141 (1-321) x PCT-US95-08743-105 (1-107)

QY 7 CAGATGACCAAGTCCATCTCCCTGCTGCTGAGAGACAGATCCATCACT 66  
Db 1 GluLeuThrGlnSerProSerSerLeuSerValGlyAspArgValThrIleThr 20  
QY 67 TGTGAGACAGTACAGACATTAGCAGCTATTAAATTGGTATCACAGAAACAGAGACG 126  
Db 21 CysArgAlaSerGlnSerIleSerSerTyrlleuAntirPyrgInGlnIlyProGlyIlys 40  
QY 127 CCTCTTAAGCTGCTATTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGACCATTC 186  
Db 41 AlaProIlySleuIleuIleTyrlAlaIleSerSerLeuGlnSerGlyValProSerArgPhe 60  
QY 187 AGTGACACGGGGTCTGGGACAGATTCACTCTCACCATCAGACAGCTCAACCTGAAGAT 246  
Db 61 SerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnProGlyIlyPro 80  
QY 247 TCTGCACTTACTACTGTACAGACAGATTACGATCCGCTACACTTTTGGCCAGGGGAC 306  
Db 81 PheAlaThrTyrlTyrlCysGlnGlnSerTyrlProGlnThrPheGlyGlnIlyThr 100  
QY 307 AAGCTGAGATCAAA 321  
Db 101 LysLeuGlnIleIlys 105

RESULT 12  
US-08-379-057-29  
Sequence 29, Application US/08379057  
Patent No. 5876950  
GENERAL INFORMATION:  
APPLICANT: Siadak, Anthony W.  
APPLICANT: Hollenbaugh, Diane L.  
APPLICANT: Gilliland, Lisa K.  
APPLICANT: Gordon, Marcia L.  
APPLICANT: Bajorath, Jürgen  
APPLICANT: Aruffo, Alejandro A.  
TITLE OF INVENTION: Monoclonal Antibodies Specific For  
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use  
TITLE OF INVENTION: In Diagnosis and Therapy  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,057  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ON0133-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 727-3670  
TELEFAX: (206) 727-3601  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-379-057-29

Alignment Scores:  
Pred. No.: 6.11e-48 Length: 108  
Score: 458.00 Matches: 89  
Percent Similarity: 88.79% Conservative: 6  
Best Local Similarity: 83.18% Mismatches: 12  
Query Match: 80.21% Indels: 0  
DB: 2 Gaps: 0

US-09-403-107-141 (1-321) x US-08-379-057-29 (1-108)

QY 1 GAGTCCAGATGACCAAGTCCATCTCCCTGCTGCTGAGAGACAGATCAC 60  
Db 1 AspleGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20  
QY 61 ATCACTGTGGAGACATTCAGACATTAGCAGCTATTAAATTGGTATTCAGACAAACCA 120  
Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrlleuAntirPyrgInGlnIlyPro 40  
QY 121 GGACGCTCTCAAGCTGCTATTACTGTGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180  
Db 41 GlySAlaProIlySleuIleuIleTyrlAlaIleSerSerLeuGlnSerGlyValProSer 60  
QY 181 CGATTCAAGTGGACGGGGTCTGGGACAGATTCACTCTCACCATCAGACAGTCTCAACT 240  
Db 61 ArgPheSerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnPro 80  
QY 241 GAAGATTCTGCACTTACTGTGACAGACAGATTACGATCCGCTACACTTTTGGCCAG 300  
Db 81 GluAspPheAlaThrTyrlTyrlCysGlnGlnSerTyrlProLeuThrPheGlyIly 100  
QY 301 GGGACCAAGCTGAGATCAAA 321  
Db 101 GlyThrIlySleuIleIlys 107

RESULT 13  
US-09-240-274-175  
Sequence 175, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 175  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-240-274-175

## Alignment Scores:

Pred. No.: 8.09e-48 Length: 107  
Score: 457.00 Matches: 87  
Percent Similarity: 90.48% Conservative: 8  
Best Local Similarity: 82.86% Mismatches: 10  
Query Match: 80.04% Indels: 0  
DB: 3 Gaps: 0

US-09-403-107-141 (1-321) x US-09-240-274-175 (1-107)

QY 7 CAGATGACCAAGTCTCCATCTCCCTGCTGCTTGTGGAGAGACAGTCAACCACT 66  
Db 2 GtLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrValThr 21  
QY 67 TGTGGCAAGTCAAGACATTAGACGCTTAAATTTGGTATACAGCAAAACAGACAG 126  
Db 22 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInySProGlyLys 41  
QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATTCACCCGGGAATCCGGGGTCCCTGACGATTC 186  
Db 42 AlaProLyLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 61  
QY 187 AGTGGACGCGGTCTGGGACAGATTTCACCTCACCATCAGACGATTCACCAAGAT 246  
Db 62 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 81  
QY 247 TGTGCAACTTACTGTCTGACGAGATTACGACATCCGTCACCTTTGGCCAGGGACC 306  
Db 82 PheAlaThrTyTrpCysGlnGlnSerTySerThrProTrpPheGlyGlnGlyThr 101  
QY 307 AAGCTGAGATCAAA 321  
Db 102 LysValGlnIleLys 106

## RESULT 14

US-09-240-274-176  
; Sequence 176, Application US/09240274  
; Patent No. 6255455

; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-09-240-274-176

## Alignment Scores:

Pred. No.: 8.09e-48 Length: 107  
Score: 457.00 Matches: 87  
Percent Similarity: 90.48% Conservative: 8  
Best Local Similarity: 82.86% Mismatches: 10  
Query Match: 80.04% Indels: 0  
DB: 3 Gaps: 0

US-09-403-107-141 (1-321) x US-09-240-274-176 (1-107)

QY 7 CAGATGACCAAGTCTCCATCTCCCTGCTGCTTGTGGAGAGACAGTCAACCACT 66  
Db 2 GtLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrValThr 21

QY 67 TGTGGCAAGTCAAGACATTAGACGCTTAAATTTGGTATACAGCAAAACAGACAG 126  
Db 22 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInySProGlyLys 41  
QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATTCACCCGGGAATCCGGGGTCCCTGACGATTC 186  
Db 42 AlaProLyLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 61  
QY 187 AGTGGACGCGGTCTGGGACAGATTTCACCTCACCATCAGACGATTCACCAAGAT 246  
Db 62 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 81  
QY 247 TGTGCAACTTACTGTCTGACGAGATTACGACATCCGTCACCTTTGGCCAGGGACC 306  
Db 82 PheAlaThrTyTrpCysGlnGlnSerTySerThrProTrpPheGlyGlnGlyThr 101  
QY 307 AAGCTGAGATCAAA 321  
Db 102 LysValGlnIleLys 106

## RESULT 15

US-09-240-274-32  
; Sequence 32, Application US/09240274  
; Patent No. 6255455

; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain 101  
US-09-240-274-32

## Alignment Scores:

Pred. No.: 1.24e-47 Length: 108  
Score: 455.50 Matches: 90  
Percent Similarity: 89.62% Conservative: 5  
Best Local Similarity: 84.91% Mismatches: 10  
Query Match: 79.77% Indels: 1  
DB: 3 Gaps: 1

US-09-403-107-141 (1-321) x US-09-240-274-32 (1-108)

QY 7 CAGATGACCAAGTCTCCATCTCCCTGCTGCTTGTGGAGAGACAGTCAACCACT 66  
Db 2 GtLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrValThr 21  
QY 67 TGTGGCAAGTCAAGACATTAGACGCTTAAATTTGGTATACAGCAAAACAGACAG 126  
Db 22 CysArgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnInySProGlyLys 41  
QY 127 CCTCCTAAGCTGCTCATTTACTGCGCATTCACCCGGGAATCCGGGGTCCCTGACGATTC 186  
Db 42 AlaProLyLeuLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgPhe 61  
QY 187 AGTGGACGCGGTCTGGGACAGATTTCACCTCACCATCAGACGATTCACCAAGAT 246  
Db 62 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyLys 81  
QY 247 TGTGCAACTTACTGTCTGACGAGATTACGACATCCGTCACCTTTGGCCAGGGG 303



Db	82	PheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProProTyrThrPheGlyGlnCly	101
QY	304	ACCAAGCTGGAGATCAAA	321
Db	102	ThrTyrLeuGlnIleLeu	107

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 Job time : 19.1474 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 300.423 Seconds

(Without alignments)  
839,678 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 571  
Sequence: 1 gagctccagatgacccagtc.....ggaccaagctggagatcaaa 321

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	Fgapop 6.0	Fgapext 7.0
	Delpop 6.0	Delpext 7.0

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 35342398

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Database : Published Applications AA.\*

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22: /cgn2\_6/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	96.1	107	14	Sequence 142, App
2	549	96.1	107	14	Sequence 149, App
3	549	96.1	214	18	Sequence 2, Appl1
4	482	84.4	107	14	Sequence 148, App
5	482	84.4	107	14	Sequence 152, App
6	468	82.0	107	10	Sequence 67, App
7	466	81.6	107	14	Sequence 104, App
8	465	81.4	107	17	Sequence 308, App
9	465	81.4	108	17	Sequence 209, App
10	464	81.3	107	10	Sequence 156, App
11	464	81.3	108	16	Sequence 4, Appl1
12	464	81.3	108	16	Sequence 28, Appl1
13	464	81.3	240	9	Sequence 2, Appl1
14	464	81.3	240	9	Sequence 2, Appl1
15	464	81.3	240	10	Sequence 2, Appl1
16	464	81.3	240	11	Sequence 2, Appl1
17	464	81.3	240	16	Sequence 1, Appl1
18	463	81.1	108	17	Sequence 2, Appl1
19	463	81.1	108	17	Sequence 2, Appl1
20	463	81.1	111	14	Sequence 2, Appl1
21	461	80.7	111	14	Sequence 2, Appl1
22	460	80.6	107	15	Sequence 2, Appl1
23	460	80.6	107	15	Sequence 2, Appl1
24	459	80.4	116	17	Sequence 2, Appl1
25	458	80.2	107	14	Sequence 2, Appl1
26	458	80.2	108	17	Sequence 2, Appl1
27	458	80.2	111	14	Sequence 2, Appl1
28	457	80.0	107	10	Sequence 2, Appl1
29	457	80.0	107	10	Sequence 2, Appl1
30	457	80.0	107	15	Sequence 2, Appl1
31	457	80.0	107	15	Sequence 2, Appl1
32	457	80.0	108	16	Sequence 2, Appl1
33	455	79.8	108	10	Sequence 2, Appl1
34	455	79.8	108	10	Sequence 2, Appl1
35	455	79.7	107	10	Sequence 2, Appl1
36	455	79.7	108	16	Sequence 2, Appl1
37	455	79.7	108	17	Sequence 2, Appl1
38	455	79.7	108	17	Sequence 2, Appl1
39	455	79.7	126	18	Sequence 2, Appl1
40	455	79.7	126	18	Sequence 2, Appl1
41	454	79.5	108	17	Sequence 2, Appl1
42	454	79.5	108	17	Sequence 2, Appl1
43	453	79.3	106	15	Sequence 2, Appl1
44	453	79.3	109	16	Sequence 2, Appl1
45	453	79.3	109	16	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-10-325-694-142  
Sequence 142, Application US/10325694  
Publication No. US200301463A1  
GENERAL INFORMATION:  
APPLICANT: KUFER, PETER  
TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN  
TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
FILE REFERENCE: 38164000  
CURRENT APPLICATION NUMBER: US/10/325,694  
CURRENT FILING DATE: 2002-12-19  
PRIOR APPLICATION NUMBER: US/09/403,107  
PRIOR FILING DATE: 1999-10-14  
NUMBER OF SEQ ID NOS: 152  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 142  
LENGTH: 107  
TYPE: PRT  
ORGANISM: HUMAN

US-10-325-694-142

## Alignment Scores:

Pred. No.:	6,05e-49	Length:	107
Score:	549.00	Matches:	105
Percent Similarity:	98.13%	Conservative:	0
Best Local Similarity:	98.13%	Mismatches:	2
Query Match:	96.15%	Indels:	0
DB:	14	Gaps:	0

US-09-403-107-141 (1-321) x US-10-325-694-142 (1-107)

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QY 1 GAGCTCCAGATGAGCCAGTCTCCATCTCCTGCTGCTTGTGGAGACAGAGTCACC 60
    |||
Db 1 GluLeuGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
QY 61 ATCACTGTGCGACAAGTCAGAGCATTTAGCAGCTATTAATAATTGATCAGCAAAACCA 120
    |||
Db 21 IleThrCysArgThrSerGlnSerIleSerSerTyLeuAsnTrpTyrglnGlnIlyPro 40
QY 121 GGAAGCTCTTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
    |||
Db 41 GlyGlnProProIysLeuLeuIleTyrrTpAlaSerThrArgIleSerGlyValProAsp 60
QY 181 CGATTGAGTGGACGGGGTCTGGGACAGATTTCACCTCCATCCAGCATCTACCAACT 240
    |||
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCAACTTACTACTGTGACAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
    |||
Db 81 GluAspSerIleThrTyrrTyrrCysGlnGlnSerTyrrAspIleProTyrrThrPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
    |||
Db 101 GlyThrIysLeuGlnIleIlys 107
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## RESULT 2

US-10-325-694-149

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/ Sequence 149, Application US/10325694
/ Publication No. US20030148463A1
/ GENERAL INFORMATION:
/ APPLICANT: KUFER, PETER
/ APPLICANT: RAUM, TOBIAS
/ TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
/ TITLE OF INVENTION: RECEPTORS AND USES THEREOF
/ FILE REFERENCE: 38164000
/ CURRENT APPLICATION NUMBER: US/10/325,694
/ CURRENT FILING DATE: 2002-12-19
/ PRIOR APPLICATION NUMBER: US/09/403,107
/ PRIOR FILING DATE: 1999-10-14
/ NUMBER OF SEQ ID NOS: 152
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 149
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: HUMAN
US-10-325-694-149
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## Alignment Scores:

Pred. No.:	6,05e-49	Length:	107
Score:	549.00	Matches:	105
Percent Similarity:	98.13%	Conservative:	0
Best Local Similarity:	98.13%	Mismatches:	2
Query Match:	96.15%	Indels:	0
DB:	14	Gaps:	0

US-09-403-107-141 (1-321) x US-10-325-694-149 (1-107)

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QY 1 GAGCTCCAGATGAGCCAGTCTCCATCTCCTGCTGCTTGTGGAGACAGAGTCACC 60
    |||
Db 1 GluLeuGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
QY 61 ATCACTGTGCGACAAGTCAGAGCATTTAGCAGCTATTAATAATTGATCAGCAAAACCA 120
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Db 21 IleThrCysArgThrSerGlnSerIleSerSerTyrrLeuAsnTrpTyrglnGlnIlyPro 40
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QY 121 GGAAGCTCTTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
    |||
Db 41 GlyGlnProProIysLeuLeuIleTyrrTpAlaSerThrArgIleSerGlyValProAsp 60
QY 181 CGATTGAGTGGACGGGGTCTGGGACAGATTTCACCTCCATCCAGCATCTACCAACT 240
    |||
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCAACTTACTACTGTGACAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
    |||
Db 81 GluAspSerIleThrTyrrTyrrCysGlnGlnSerTyrrAspIleProTyrrThrPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
    |||
Db 101 GlyThrIysLeuGlnIleIlys 107
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## RESULT 3

US-10-778-915-2

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/ Sequence 2, Application US/10778915
/ Publication No. US20050180979A1
/ GENERAL INFORMATION:
/ APPLICANT: PETERS, MALTE
/ APPLICANT: LOCHER, MATTHIAS
/ APPLICANT: PRANG, NADJA
/ APPLICANT: QUADT, CORNELIA
/ TITLE OF INVENTION: Anti-BpCAM Immunoglobulins
/ FILE REFERENCE: DEBE:031US
/ CURRENT APPLICATION NUMBER: US/10/778,915
/ CURRENT FILING DATE: 2004-02-13
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 214
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Synthetic Peptide
US-10-778-915-2
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## Alignment Scores:

Pred. No.:	6,59e-49	Length:	214
Score:	549.00	Matches:	105
Percent Similarity:	98.13%	Conservative:	0
Best Local Similarity:	98.13%	Mismatches:	2
Query Match:	96.15%	Indels:	0
DB:	18	Gaps:	0

US-09-403-107-141 (1-321) x US-10-778-915-2 (1-214)

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Db 1 GluLeuGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20
QY 61 ATCACTGTGCGACAAGTCAGAGCATTTAGCAGCTATTAATAATTGATCAGCAAAACCA 120
    |||
Db 21 IleThrCysArgThrSerGlnSerIleSerSerTyrrLeuAsnTrpTyrglnGlnIlyPro 40
QY 121 GGAAGCTCTTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
    |||
Db 41 GlyGlnProProIysLeuLeuIleTyrrTpAlaSerThrArgIleSerGlyValProAsp 60
QY 181 CGATTGAGTGGACGGGGTCTGGGACAGATTTCACCTCCATCCAGCATCTACCAACT 240
    |||
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCAACTTACTACTGTGACAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
    |||
Db 81 GluAspSerIleThrTyrrTyrrCysGlnGlnSerTyrrAspIleProTyrrThrPheGlyGln 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
    |||
```

DB 101 Glythrlvbleuglilelys 107  
RESULT 4  
US-10-325-694-148  
; Sequence 148, Application US/10325694  
; Publication No. US20030148463A1  
; GENERAL INFORMATION:  
; APPLICANT: KUFER, PETER  
; APPLICANT: RAUM, TOBIAS  
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN  
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
; FILE REFERENCE: 38164000  
; CURRENT APPLICATION NUMBER: US/10/325,694  
; PRIOR APPLICATION NUMBER: US/09/403,107  
; PRIOR FILING DATE: 1999-10-14  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 148  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-10-325-694-148  
Alignment Scores:  
Pred. No.: 6.7e-42 Length: 107  
Score: 482.00 Matches: 92  
Percent Similarity: 92.52% Conservative: 7  
Best Local Similarity: 85.98% Mismatches: 8  
Query Match: 84.41% Indels: 0  
DB: 14 Gaps: 0  
US-09-403-107-141 (1-321) x US-10-325-694-148 (1-107)  
QY 1 GAGCTCCAGATGACCCAGCTCCATCTCCCTGCTGCTGAGAGACAGATCACC 60  
DB 1 GluleuglmetrlnglnserProserSerleuseralaserValGlyAspArgValThr 20  
QY 61 ATCACTTGTCGACAGATGACAGATTGACGACTTAAATTGGTATCAGCAAAACA 120  
DB 21 lIethrCysArgAlaserGlnserlIeserlSerlryrleuAenrrpyrGlnGlnlyPro 40  
QY 121 GGACAGCCTCCTAAGCTGCTCATTACTGCGATTCACCCGGGATCCGGGCTCCCTAC 180  
DB 41 GlylnProProlyrleuLeuiletyrtrpAlaserThrArgGlnSerGlyValProasp 60  
QY 181 CGATTCACTGCGACGGGCTGCGAGAGATTTCATCTCACCATCAGCAGCTCAACCT 240  
DB 61 ArgPheSerGlySerGlnserGlyThrAsnrryrrhrleuThrIleSerSerleuglnPro 80  
QY 241 GAAGATTCTGCACTTACTACTGTCAGCAGAGATTGACGACATCCCGTACACTTTGGCCAG 300  
DB 81 GluAspPheAlatrThrPheCysGlnGlnIleSerAspSerleuProIleThrPheGlyln 100  
QY 301 GGGACCAAGCTCGAGATCAAA 321  
DB 101 GlyThrArgLeuAspIleGln 107  
RESULT 5  
US-10-325-694-152  
; Sequence 152, Application US/10325694  
; Publication No. US20030148463A1  
; GENERAL INFORMATION:  
; APPLICANT: KUFER, PETER  
; APPLICANT: RAUM, TOBIAS  
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN  
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
; FILE REFERENCE: 38164000  
; CURRENT APPLICATION NUMBER: US/10/325,694  
; PRIOR APPLICATION NUMBER: US/09/403,107  
; PRIOR FILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 152  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-10-325-694-152  
Alignment Scores:  
Pred. No.: 6.7e-42 Length: 107  
Score: 482.00 Matches: 92  
Percent Similarity: 92.52% Conservative: 7  
Best Local Similarity: 85.98% Mismatches: 8  
Query Match: 84.41% Indels: 0  
DB: 14 Gaps: 0  
US-09-403-107-141 (1-321) x US-10-325-694-152 (1-107)  
QY 1 GAGCTCCAGATGACCCAGCTCCATCTCCCTGCTGCTGAGAGACAGATCACC 60  
DB 1 GluleuglmetrlnglnserProserSerleuseralaserValGlyAspArgValThr 20  
QY 61 ATCACTTGTCGACAGATGACAGATTGACGACTTAAATTGGTATCAGCAAAACA 120  
DB 21 lIethrCysArgAlaserGlnserlIeserlSerlryrleuAenrrpyrGlnGlnlyPro 40  
QY 121 GGACAGCCTCCTAAGCTGCTCATTACTGCGATTCACCCGGGATCCGGGCTCCCTGAC 180  
DB 41 GlylnProProlyrleuLeuiletyrtrpAlaserThrArgGlnSerGlyValProasp 60  
QY 181 CGATTCACTGCGACGGGCTGCGAGAGATTTCATCTCACCATCAGCAGCTCAACCT 240  
DB 61 ArgPheSerGlySerGlnserGlyThrAsnrryrrhrleuThrIleSerSerleuglnPro 80  
QY 241 GAAGATTCTGCACTTACTACTGTCAGCAGAGATTGACGACATCCCGTACACTTTGGCCAG 300  
DB 81 GluAspPheAlatrThrPheCysGlnGlnIleSerAspSerleuProIleThrPheGlyln 100  
QY 301 GGGACCAAGCTCGAGATCAAA 321  
DB 101 GlyThrArgLeuAspIleGln 107  
RESULT 6  
US-09-791-153A-67  
; Sequence 67, Application US/09791153A  
; Publication No. US20030103978A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Hitz, Anna  
; APPLICANT: Boyle, William  
; APPLICANT: Sullivan, John  
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN  
; FILE REFERENCE: A-633A  
; CURRENT APPLICATION NUMBER: US/09/791,153A  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/511,139  
; PRIOR FILING DATE: 2000-02-23  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-153A-67  
Alignment Scores:  
Pred. No.: 1.98e-40 Length: 107  
Score: 468.00 Matches: 90  
Percent Similarity: 90.65% Conservative: 7  
Best Local Similarity: 84.11% Mismatches: 10  
Query Match: 81.96% Indels: 0  
DB: 10 Gaps: 0

US-09-403-107-141 (1-321) x US-09-791-153A-67 (1-107)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGTGGAGACAGAGTCACC 60  
Db 1 AspIleGImetHrGInSerProSerSerLeuSerValGlyAspArgValThr 20  
QY 61 ATCACTTGTGGCAAGATGACAGCATTTAGCAGCATTAATTAATGATATCAGAGAAACA 120  
Db 21 lIeThrCyArGInSerGInSerIleSerSerTyRleuAsnTrpYrGInGlnuYrPro 40  
QY 121 GACAGCTCTTAGCTGCTCATTTACTGCGCATTAACCGGAAATCCGGGATCCCTGAC 180  
Db 41 GlyLeuAlaProLysLeuIleuIleTyRAlaAlaSerSerLeuGInSerGlyValProSer 60  
QY 181 CGATTGAGTGGACGGGCTGTGGAGAGATTTCATCTCCATCCATCAGAGTCACCAACT 240  
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGInPro 80  
QY 241 GAAGATTCTGCACTTACTGCTGACAGAGATTACAGACATCCCGTACACTTTGGCCAG 300  
Db 81 GluAspPheAlaThrTyRTrpYrGInGInSerTySerThrProTrpThrPheGlyGln 100  
QY 301 GGGACCAAGCTGGAGATCAA 321  
Db 101 GlyThrIleValGluIleLys 107

## RESULT 7

US-10-016-986-104  
; Sequence 104, Application US/10016986  
; Publication No. US20030187247A1  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbos, Carlos R  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; FILE REFERENCE: 313.2CON1  
; CURRENT APPLICATION NUMBER: US/10/016,986  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 09/149,898  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: US 08/899,575  
; PRIOR FILING DATE: 1997-07-24  
; PRIOR APPLICATION NUMBER: US 08/276,852  
; PRIOR FILING DATE: 1994-07-18  
; PRIOR APPLICATION NUMBER: US 08/178,302  
; PRIOR FILING DATE: 1994-01-06  
; PRIOR APPLICATION NUMBER: PCT/US93/09328  
; PRIOR FILING DATE: 1993-09-30  
; PRIOR APPLICATION NUMBER: US 07/954,148  
; PRIOR FILING DATE: 1992-09-30  
; NUMBER OF SEQ ID NOS: 176  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 104  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized  
US-10-016-986-104

Alignment Scores:  
Pred. No.: 3,22e-40 Length: 107  
Score: 466.00 Matches: 90  
Percent Similarity: 90.48% Conservative: 5  
Best Local Similarity: 85.71% Mismatches: 10  
Query Match: 81.61% Indels: 0  
Gaps: 0

US-09-403-107-141 (1-321) x US-10-016-986-104 (1-107)

QY 7 CAGATGACCAAGTCTCCATCTCCCTGCTCTCTGTGGAGACAGAGTCACCACTACT 66  
Db 1 AspIleGImetHrGInSerProSerSerLeuSerValGlyAspArgValThr 20

Db 1 GluLeuThrGInSerProSerSerLeuSerValGlyAspArgValThrIleThr 20

QY 67 TGTGGACAGATGACAGCATTTAGCAGCATTAATTAATGATATCAGAGAAACAAGAGCAG 126  
Db 21 CysArgAlaSerGInSerIleSerSerTyRleuAsnTrpYrGInGlnuYrProGlyLys 40  
QY 127 CCTCCAGCTGCTCATTTACTGCGCATTAACCGGAAATCCGGGATCCCTGACCATTC 186  
Db 41 AlaProLysLeuIleuIleTyRAlaAlaSerSerLeuGInSerGlyValProSerArgPhe 60  
QY 187 AGTGGACGGGCTGTGGAGAGATTTCATCTCCATCCATCAGAGTCACCAACTGAAGT 246  
Db 61 SerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGInProGlnuYr 80  
QY 247 TCTGCACTTACTGCTGACAGAGATTACAGACATCCCGTACACTTTGGCCAGGGAGCC 306  
Db 81 PheAlaThrTyRTrpYrGInGInSerTySerThrProTyRThrPheGlyGlnuYrThr 100  
QY 307 AAGCTGGAGATCAA 321  
Db 101 LysLeuGluIleLys 105

## RESULT 8

US-10-727-155-308  
; Sequence 308, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspel S. Kang  
; APPLICANT: Orit Foord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendescho  
; APPLICANT: Palaniswami Rathnaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Raffaella Faggioli  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: ABGENIX.073A  
; CURRENT APPLICATION NUMBER: US/10/727,155  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 308  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-308

Alignment Scores:  
Pred. No.: 4.1e-40 Length: 107  
Score: 465.00 Matches: 90  
Percent Similarity: 89.72% Conservative: 6  
Best Local Similarity: 84.11% Mismatches: 11  
Query Match: 81.44% Indels: 0  
Gaps: 0

US-09-403-107-141 (1-321) x US-10-727-155-308 (1-107)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTCTCTGTGGAGACAGAGTCACC 60  
Db 1 AspIleGImetHrGInSerProSerSerLeuSerValGlyAspArgValThr 20  
QY 61 ATCACTTGTGGCAAGATGACAGCATTTAGCAGCATTAATTAATGATATCAGAGAAACA 120



```

FILE REFERENCE: 8039/2032
CURRENT APPLICATION NUMBER: US/10/409,814A
CURRENT FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-10-409-814A-4

Alignment Scores:
Pred. No.: 5,23e-40      Length: 108
Score: 464.00          Matches: 90
Percent Similarity: 89.72%      Conservative: 6
Best Local Similarity: 84.11%    Mismatches: 11
Query Match: 81.26%             Indels: 0
DB: 16                         Gaps: 0

US-09-403-107-141 (1-321) x US-10-409-814A-4 (1-108)

QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCTGCTGCTTCTGTGGAGACAGATCAC 60
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20

QY 61 ATACTCTTGCGGCAAGTCAGACGATTCACGACTTAAATGGTATCACGAAACCA 120
Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyLeuAsnTyrGlnGlnLysPro 40

QY 121 GGACAGCCTCTCTAAGCTGCTCATTTTACGTGGCAGATCTACCCGGGATCCGGGGTCCCTGAC 180
Db 41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60

QY 181 CGATTTCAGTGGCAGCGGGTCTGGAGACAGATTTCACCTTCACCATGACAGTCTCAACT 240
Db 61 ArgPheSerIlySerGlySerGlyThrAspPheThrIleThrIleSerSerLeuGlnPro 80

QY 241 GAAGATTCTGCAACTTACTACTGTCCAGACAGATTACGACATCCGGTACACTTTTGAGCAG 300
Db 81 GlnAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProAsnThrPheGlyGln 100

QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 101 GlyThrIysValGlnIleLys 107

RESULT 12
US-10-726-332-28
/ Sequence 28, Application US/10726332
/ Publication No. US2005058649A1
/ GENERAL INFORMATION:
/ APPLICANT: Gregory M. Landes
/ APPLICANT: Mary Haak-Frendscho
/ APPLICANT: Ling Chen
/ APPLICANT: Yen-Wah R. Lee
/ APPLICANT: Meina Liang
/ APPLICANT: Xiao Feng
/ APPLICANT: Xiao-Chi Jia
/ APPLICANT: Mark R. Nocerini
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
/ FILE REFERENCE: AGENIX.07A
/ CURRENT APPLICATION NUMBER: US/10/726,332
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: n/a
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 222
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 28
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-726-332-28

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Alignment Scores:		Pred. No.: 5	23e-40	Length: 108
Score:	464.00	Matches:	90	
Percent Similarity:	90.65%	Conservative:	7	
Best Local Similarity:	84.11%	Mismatches:	10	
Query Match:	81.26%	Indels:	0	
DB:	17	Gaps:	0	
US-09-403-107-141 (1-321) x US-10-726-332-28 (1-108)				
QY	1	GAGCTCCAGATGACCCAGTCTCCATCTCCTGTCTGCTTTCTGGGAGACAGTACC	60	
DB	1	AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	20	
QY	61	ATCACTTGTCGGACAGTACGAGCAATTGGACGCTTTAAATTGGTATCGACGAACA	120	
DB	21	IleThrCysArgAlaSerIleSerIleSerSerIleuAsnThrPyrGlnGlnLysPro	40	
QY	121	GSACAGCCCTCTAGAGTGCCTATTACTGGACATCTACCCGGAAATCCGGGCTCCCTGAC	180	
DB	41	GlyAlaSerProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyAlaProSer	60	
QY	181	CGATTACGTGGACGCGGGTCTGGACAAATTTCACTTCACCATACGACAGTCTAACCT	240	
DB	61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80	
QY	241	GAAGATTCTGCACCTTACACTACGTACGACGAGATTACGACATCCCGTACACTTTGGCCAG	300	
DB	81	GlnAspPheAlaThrTyrTyrCysGlnGlnSerIleTyrAsnThrProPheThrPheGlyGln	100	
QY	301	GGGACCAAGCTGGAGATCAA 321		
DB	101	GlyThrLysValGluIleLys 107		
RESULT 13				
US-09-192-854-2				
Sequence 2, Application US/09192854				
Patent No. US20020068276A1				
GENERAL INFORMATION:				
APPLICANT: Winter, Greg				
APPLICANT: Tomlinson, Ian				
TITLE OF INVENTION: Methods for Selecting Functional Peptides				
FILE REFERENCE: 3789/72916				
CURRENT APPLICATION NUMBER: US/09/192,854				
CURRENT FILING DATE: 1998-11-17				
EARLIER APPLICATION NUMBER: 60/066,729				
EARLIER FILING DATE: 1997-11-21				
NUMBER OF SEQ ID NOS: 212				
SOFTWARE: PatentIn Ver. 2.0				
SEQ ID NO 2				
LENGTH: 240				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-09-192-854-2				
Alignment Scores:				
Pred. No.:	5	78e-40	Length: 240	
Score:	464.00	Matches:	90	
Percent Similarity:	89.72%	Conservative:	6	
Best Local Similarity:	84.11%	Mismatches:	11	
Query Match:	81.26%	Indels:	0	
DB:	9	Gaps:	0	
US-09-403-107-141 (1-321) x US-09-192-854-2 (1-240)				
QY	1	GAGCTCCAGATGACCCAGTCTCCATCTCCTGTCTGCTTTCTGGGAGACAGTACC	60	
DB	133	AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	152	
QY	61	ATCACTTGTCGGACAGTACGAGCAATTGGACGCTTTAAATTGGTATCGACGAACA	120	
DB	153	IleThrCysArgAlaSerIleSerIleSerSerIleuAsnThrPyrGlnGlnLysPro	172	



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QY 121 GGACGACCTCCCTAGGCTGCTCATTTACTTGGGAGATCTAACCCGGGAATCCGGGGCTCCCTGAC 180
Db 173 GtlyvAlProlylsneuulIeTyAlAlaserIeuGlnSerGlyValProSer 192
QY 181 CGATTTCAGTGGACCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCAACT 240
Db 193 ArgPheSerGlySerGlySerGlyThrAspPheThrIeuThrIeSerSerIeuGlnPro 212
QY 241 GAAGATTTGGCAACTTACTACTGTCCAGCAGAGTTTACGACATCCCGTACACTTTGGCCAG 300
Db 213 GluAspPheAlaThrTyTCysGlnGlnSerTySerThrProAnthrPheGlyGln 232
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 233 GlyThrLysValGlnIleLys 239

RESULT 14
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Patent No. US2002016462A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-968-561A-2

Alignment Scores:
Pred. No.: 5,78e-40 Length: 240
Score: 464.00 Matches: 90
Percent Similarity: 89.72% Conservative: 6
Best Local Similarity: 84.11% Mismatches: 11
Query Match: 81.26% Indels: 0
DB: 9 Gaps: 0

US-09-403-107-141 (1-321) x US-09-968-561A-2 (1-240)
QY 1 GAGCTCCAGATGAGCCAGTCTCCATCTCCCTGTGCTTCTGTGGAGACAGAGTACC 60
Db 133 AsplIeGlnMerThrGlnSerProSerSerIeuSerAlaSerValGlyAspArgValThr 152
QY 61 ATCACTTGTCCGACAGAGTCCAGAGCATTTAGACGCTATTAAATGGTATTCAGCAAAACCA 120
Db 153 IleThrCysArgAlaSerGlnSerIleSerSerTyIeuAntPrTyGlnGlnLysPro 172
QY 121 GGACGACCTCCCTAGGCTGCTCATTTACTGTCCGATCTCCCGGGAATCCGGGGTCCCTGAC 180
Db 173 GtlyvAlProlylsneuulIeTyAlAlaserIeuGlnSerGlyValProSer 192
QY 181 CGATTTCAGTGGACCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCAACT 240
Db 193 ArgPheSerGlySerGlySerGlyThrAspPheThrIeuThrIeSerSerIeuGlnPro 212
QY 241 GAAGATTTGGCAACTTACTACTGTCCAGCAGAGTTTACGACATCCCGTACACTTTGGCCAG 300
Db 213 GluAspPheAlaThrTyTCysGlnGlnSerTySerThrProAnthrPheGlyGln 232

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Db      213 GluAepPhaLaThrYrYrCySGInGInSerTySerThrProAnThrPhGcIyGln 232
Qy      301 GGGACCAAGCTGGAGATCAAA 321
      |||||:::|||||
Db      233 GlyThrIysValGlnIleIys 239

RESULT 15
US-09-968-744A-2
; Sequence 2, Application US/0968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; PRIORITY FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-2

Alignment Scores:
Pred. No.: 5,78e-40 Length: 240
Score: 464.00 Matches: 90
Percent Similarity: 89.72% Conservative: 6
Best Local Similarity: 84.11% Mismatches: 11
Query Match: 81.26% Indels: 0
DB: 10 Gaps: 0

US-09-403-107-141 (1-321) x US-09-968-744A-2 (1-240)
Qy      1 GAGCTCAGATGATGACCAAGCTCCATCTCCCTGTCGTTCTGNGGAGACAGAGTCACC 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      133 AapIleGInMeThrGInSerProSerSerIleuSerAlaSerValGlyAepPhaValThr 152
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy      61 ATCACTGTGCGACAAAGTCAGAGCATTTAGCAGCTATTAAATTGTTATCAGACAGAAACA 120
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      153 IleThrCySArGAlaSerGInSerIleSerIleSerTyIleuAnThrTyGInGInIlyPro 172
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy      121 GGAAGACCTCCCTTAAGTGTCTCATTTACTGGCAATCAACCGGAAATCCGGGGTCCCTGAC 180
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      173 GlyIysAlaProIyIleuIleuIleTyAlaAlaSerSerIleuGInSerGlyValProSer 192
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy      181 GGAATTCAGTGGAGCGGGGTCTGGGACAGATTTCACTTCACATCCAGTCAGAGCTTCAACT 240
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      193 ArgPheSerGlySerGlySerGlyIleThrIlePheThrIleuThrIleSerSerIleuGInPro 212
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy      241 GAAGATTCTGCAACTTACTACTGTCTAGCAGAGATTACAGCAATCCGCTTACACTTTTGGCCAG 300
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      213 GluAepPhaLaThrYrYrCySGInGInSerTySerThrProAnThrPhGcIyGln 232
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy      301 GGGACCAAGCTGGAGATCAAA 321
      |||||:::|||||
Db      233 GlyThrIysValGlnIleIys 239

```

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GenCore version 5.1.6  
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## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 14.4038 Seconds

(without alignments)  
4288.519 Million cell updates/sec

Title: US-09-403-107-141

Perfect score: 571  
Sequence: 1 gagctccagatgacccagtc.....ggaccaagcggagatcaaa 321

## Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-O=/cgn2.1/USPRO.epool.p/US09403107/runat.29082005.120125.18902/app\_query.fasta.1.1038  
-DB=PIR -QFMT=fastlan -SUPFIX=irp -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLALIGN=200 -THR.SCOR=spct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=spc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09403107@cgn.1.1.77@runat.29082005.120125.18902 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG.SCOR=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

PIR\_79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	464	81.3	123	2	S40331
2	463	81.1	109	2	S31981
3	462	80.9	127	2	S40367
4	460	80.6	109	2	S31998
5	458	80.2	108	2	B49047
6	451	79.0	108	2	S47182
7	450	78.8	129	1	KIHUWK
8	449	78.5	109	2	S31978
9	448	78.5	129	2	S52792
10	446	78.1	108	2	S44122
11	445	77.9	109	2	S31979
12	441	77.2	108	2	S19674
13	441	77.2	109	2	S31980
14	438	76.7	120	2	S46370

15	437	76.5	108	2	S31977	Ig kappa chain - h
16	437	76.5	117	2	S46371	Ig kappa chain V-J
17	436	76.4	108	1	KIHUHU	Ig kappa chain V-I
18	436	76.4	129	2	S40317	Ig kappa chain - h
19	435	76.2	109	2	S31983	Ig kappa chain - h
20	435	76.2	114	1	K4HULN	Ig kappa chain V-I
21	435	76.2	129	2	S52793	Ig kappa chain V r
22	434	76.0	107	2	S36264	Ig kappa chain V
23	433.5	75.9	125	2	S40315	Ig kappa chain - h
24	433	75.8	108	1	KIHULY	Ig kappa chain V-I
25	433	75.8	125	2	S40333	Ig kappa chain V-J
26	432.5	75.7	107	2	S36275	Ig kappa chain V
27	432	75.7	109	2	S32001	Ig kappa chain - h
28	432	75.7	125	2	S40350	Ig kappa chain - h
29	428	75.0	107	2	S36268	Ig kappa chain V
30	428	75.0	122	2	S40370	Ig kappa chain - h
31	428	75.0	131	2	S40352	Ig kappa chain V-J
32	425	74.4	113	2	S34002	Ig kappa chain V r
33	424	74.3	108	1	KIHUDE	Ig kappa chain V-I
34	424	74.3	126	2	S40335	Ig kappa chain V-J
35	423	74.1	128	2	S46372	Ig kappa chain var
36	422.5	74.0	108	2	S30521	Ig kappa chain V r
37	422	73.9	107	2	S36269	Ig kappa chain V
38	422	73.9	108	1	KIHURE	Ig kappa chain V-I
39	422	73.9	129	2	I39154	Ig kappa chain (BR
40	422	73.9	129	2	S52789	Ig kappa chain V r
41	422	73.9	134	1	K4HUI7	Ig kappa chain pre
42	421	73.7	108	1	KIHUUV	Ig kappa chain V-I
43	421	73.7	120	2	S51147	antibody light cha
44	420	73.6	108	1	KIHOUU	Ig kappa chain V-I
45	420	73.6	129	2	S40369	Ig kappa chain - h

## ALIGNMENTS

RESULT 1  
S40331  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40331  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40331  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-123 <KLB>  
A/Cross-References: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:9441351  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/32-106/Domain: immunoglobulin homology <IMW>

## Alignment Scores:

Pred. No.:	2,41e-34	Length:	123
Score:	464.00	Matches:	90
Percent Similarity:	89.72%	Conservative:	6
Best Local Similarity:	84.11%	Mismatches:	11
Query Match:	81.26%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x S40331 (1-123)

QY	1	GAGCTCCAGTACGACCCAGTCCATCCCTGCTGCTTCTGTGGAGACAGATCACC	60
DB	17	AspIeGlnMetThrGlnSerProSerSerLeuSerLaserValGlyAspArgValThr	36
QY	61	ATCACTTGTGGACCAAGTCAAGACATTAGCAGCTATTAAATTGATTCAGCAACCA	120
DB	37	IleThrCysArgLysSerGlnSerIleSerSerTyrLeuAsnTyrGlnGlnTyrPro	56
QY	121	GGAGAGCTCTTAAGCTGCTCATTTACTGGGAGTCTACCGGGAATCCGGGGTCCCTGAC	180

Db 57 GYLVALAPRQYLSLEULEILEYTRALALASERISERLEUGINSERGLVALPRSer 76

QY 181 CGATTAGAGCGACGGGTCTGGGACAGATTTCATCTCACCATCAGCAGCTCAAACT 240

Db 77 ACPHESERGLYSERISYSERGLYMRAPHEINRLEUTHRILESERLEUGINPro 96

QY 241 GAAGATTTCGCAACTACTACTGTGACGAGATTACGACATCCGGTACACTTTGGCAG 300

Db 97 GLHAPHEIALATHRYTRYCYSGINGINSERYISERHPROARGTHRPHEGLYGLN 116

QY 301 GGGACCAAGCTGAGATCAAA 321

Db 117 GLYTHRLYSVALGLNILEYLS 123

```

RESULT 2
S31981
IG kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31981
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McRachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31981
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <PDB>
A/Cross-References: EMBL:Z15077, NID:G38493, PIDD:CA4786.1, PID:G38494
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
C/16-90/Domain: immunoglobulin homology <IMM>

```

Predictive Decoys:	
Pred. No.:	3,01e-34
Score:	463.00
Percent Similarity:	87.85%
Best Local Similarity:	85.05%
Query Match:	81.09%
DB:	2
Gaps:	0
Indels:	0
Mismatches:	13
Conservative:	3
Matches:	91
Length:	109

US-09-403-107-141 (1-321) x S31981 (1-109)

Qy	I	GAGCTCCAGATATACCCAGAGCTCCATCTCCCTCTGCTTCGTGGGAGAGAGTACC	60
Db	1	GluLeuValMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	20
Qy	61	ATCACTTGTTCGACAAGTCAGAGCATTTACAGACTATTAATTTGGTATCAGCAGAAACA	120
Db	21	IleThrCysArgAlaSerGlnAspIleSerArgIlyLeuAsnTrpTyrGlnGlnIlyPro	40
Qy	121	GGACAGCCCTCAAGCTGTCATTTATCTGGCATCTACCCGGAGATCCGGGGTCCCTGAC	180
Db	41	GlyValAsnAlaProIysLeuLeuIleHisGlyAlaSerThrLeuGlnSerGlyValProGly	60
Qy	181	CGATTCAGTGGACGGCGGTCTGGGACAGATTTCACTTCACCATCAGACGATCTCAAACT	240
Db	61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80
Qy	241	GAGGATCTTCACATCTACTGTCGACGAGAGTTGACGATCCGCTGATCTTTGGCCAG	300
Db	81	GluAspArgAlaThrTyrTyrCysGlnGlnSerTyrSerThrProPheThrPheGlyGln	100
Qy	301	GGGACCAAGCTGGAGATCAAA	321
Db	101	GlyThrIysLeuGlnIleIlys	107

```

RESULT 3
S40367
IG kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_reviston 26-May-1995 #text_change 21-Jan-2000

```

C:Accession: S40367  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Err. J. Immunol. 23, 3246-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40367  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-127 <KLE>  
A:Cross-references: EMBL:X72477  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:33-107/Domain: immunoglobulin homology <Imm>

Alignment Scores:	
Pred. No.:	3.64e-34
Score:	462.00
Percent Similarity:	91.59%
Best Local Similarity:	82.24%
Query Match:	80.91%
DB:	2
Length:	127
Matches:	88
Conservative:	8
Mismatches:	9
Indels:	1
Gaps:	0

US-09-403-107-141 (1-321) X S40367 (1-127)

[illegible]

QY 301 GGGACCAAGCTGGAGATCAA 321  
 |||||:::|||||  
 Db 118 GlyThrLysValGluIleLys 124

RESULT 4  
S31998  
Ig kappa chain - human (fragment)  
C.Species: Homo sapiens (man)  
C.Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
R.Portfolio: S31998  
R.Accession: S31998  
submitted to the EMBL Data Library, June 1992  
A.Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A.Reference number: S31977  
A.Accession: S31998  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-109 <PDB>  
A.Cross-References: EMBL:Z15081; NID:G38501; PIDD:CA478790.1; PID:G38502  
C.Superfamily: immunoglobulin V region; immunoglobulin homology  
C.Keywords: heterotrimer; immunoglobulin  
F.16-90/Domain: immunoglobulin homology <IMM>

Prd. No.:	5.64e-34	Length:	106
Score:	460.00	Matches:	89
Percent Similarity:	89.72%	Conservative:	7
Best Local Similarity:	83.18%	Mismatches:	11
Query Match:	80.56%	Indels:	0





Db 43 IleThrCysArgAlaSerGlnSerIleAlaGlyTyrLeuAsnTrpTyrGlnGlnArgPro 62  
Qy 121 GGACGCTCTTAAGCTGCTCATTTACTGGCGATTCACCCGGGAATCCGGGGTCTCTGAC 180  
Db 63 GlyValAlaProGlnLeuLeuIleTyrAlaAlaSerThrLeuArgSerGlyValProSer 82  
Qy 181 CGATTCAGTGGGAGGGGCTGGGACAGATTTCATCTCCACCATAGAGAGTCTCAACCT 240  
Db 83 ArgPheSerGlySerGlySerGlyValAlaPheThrLeuThrIleSerSerLeuGlnPro 102  
Qy 241 GAAGATTCGCAACTTACTACTGTGAGCAGAGTTACGATCCCGTACACTTTTGGCCAG 300  
Db 103 GluAspSerAlaIleTyrTyrCysGlnGlnInsertyrGlyThrProPheThrPheGlyPro 122  
Qy 301 GGGACCAAGCTGGAGATCAAA 321  
Db 123 GlyThrLysValAlaPheIleLys 129

## RESULT 10

S44122  
Ig kappa chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C/Accession: S44122  
R/Hawkins, R.E.; Zhu, D.; Owecke, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A/Description: Idiolytic vaccination against human B-cell lymphoma: rescue of variable  
A/Reference number: S44105  
A/Accession: S44122  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-108 <HW>  
A/Cross-references: EMBL:Z13190, NID:9472976, PIDN:CAA83265.1, PID:9340533  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/16-90/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1.05e-32	Length:	108
Score:	446.00	Matches:	87
Percent Similarity:	87.85%	Conservative:	7
Best Local Similarity:	81.31%	Mismatches:	13
Query Match:	78.11%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x S44122 (1-108)

Qy 1 GAGCTCCAGATGACCCAGCTCCATCTCCCTGCTGCTGCTGGGAGAGATCAC 60  
Db 1 AsplIegImeThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
Qy 61 ATCACTTGTCGACAAAGTCAGAGATTAGAGCTATTAATTTGGTATCAGCAAAACA 120  
Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysLeu 40  
Qy 121 GGACGCTCTTAAGCTGCTCATTTACTGGCGATTCACCCGGGAATCCGGGGTCTCTGAC 180  
Db 41 GlyValAlaProGlnLeuLeuIleTyrAlaAlaSerThrLeuArgSerGlyValProSer 60  
Qy 181 CGATTCAGTGGGAGGGGCTGGGACAGATTTCATCTCCACCATAGAGAGTCTCAACCT 240  
Db 61 ThrPheSerGlySerGlySerGlyValAlaPheThrLeuThrIleSerSerLeuGlnPro 80  
Qy 241 GAAGATTCGCAACTTACTACTGTGAGCAGAGTTACGATCCCGTACACTTTTGGCCAG 300  
Db 81 GluAspSerAlaIleTyrTyrCysGlnGlnInsertyrSerThrProTrpThrPheGlyPro 100  
Qy 301 GGGACCAAGCTGGAGATCAAA 321  
Db 101 GlyThrLysValAlaPheIleLys 107

## RESULT 11

S31979

Ig kappa chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S31979  
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A/Reference number: S31977  
A/Accession: S31979  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-109 <POR>  
A/Cross-references: EMBL:Z15075, NID:938489, PIDN:CAA78784.1, PID:938490  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/16-90/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1.3e-32	Length:	109
Score:	445.00	Matches:	86
Percent Similarity:	86.92%	Conservative:	7
Best Local Similarity:	80.37%	Mismatches:	14
Query Match:	77.93%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) x S31979 (1-109)

Qy 1 GAGCTCCAGATGACCCAGCTCCATCTCCCTGCTGCTGCTGGGAGAGATCAC 60  
Db 1 GluValMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
Qy 61 ATCACTTGTCGACAAAGTCAGAGATTAGAGCTATTAATTTGGTATCAGCAAAACA 120  
Db 21 IleSerCysArgAlaSerGlnSerIleGlyLysTyrLeuAsnTrpTyrArgGlnLysPro 40  
Qy 121 GGACGCTCTTAAGCTGCTCATTTACTGGCGATTCACCCGGGAATCCGGGGTCTCTGAC 180  
Db 41 GlyValAlaProGlnLeuLeuIleTyrGlyThrSerThrLeuGlnSerGlyValProSer 60  
Qy 181 CGATTCAGTGGGAGGGGCTGGGACAGATTTCATCTCCACCATAGAGAGTCTCAACCT 240  
Db 61 ArgPheSerGlySerGlyPheGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
Qy 241 GAAGATTCGCAACTTACTACTGTGAGCAGAGTTACGATCCCGTACACTTTTGGCCAG 300  
Db 81 GluAspPheAlaThrTyrPheCysGlnGlnInsertyrSerSerProTyrThrPheGlyPro 100  
Qy 301 GGGACCAAGCTGGAGATCAAA 321  
Db 101 GlyThrLysLeuGlnIleLys 107

## RESULT 12

S19674  
Ig kappa chain V region (clone alpha-TEU) - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C/Accession: S19674  
R/Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.; Mol. Biol. 222, 581-597, 1991  
A/Title: BV-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A/Reference number: S19663; PMID:92085276; PMID:1748994  
A/Accession: S19674  
A/Molecule type: mRNA  
A/Residues: 1-108 <MAR>  
A/Cross-references: EMBL:X61642, NID:937860, PIDN:CAA43823.1, PID:91335386  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/16-90/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	3e-32	Length:	108
Score:	441.00	Matches:	86
Percent Similarity:	86.92%	Conservative:	7

Best Local Similarity:	80.37%	Mismatches:	14
Query Match:	77.23%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) X S19674 (1-108)

Oy	GAGTCCGAATACCCAGATCTCCATCTCCGTGCTTCGTGGGAGACAGATACC	60
	:::	
Oy	1	
Db	GIUIIEVALLIETHNRHINSEPRSESRSEIUSERHLASERVALGIYASPRYVALTHR	20
Oy	ATCATCTTGTCCGACAAATCCAGACATTTCAGACCTATTTAAATTGGTATCAGCAAAACA	120
	:::	
Db	1	
Db	ILETHRYASRGLASERGINSEIRLIESEAAIYRLIEMASTRIPLYGILNHLYPEPRO	40
Oy	GGACAGCCCTCTTAAGCTGCATTTACTGGACATTCACCCGGGAATCCGGAGTCCCTGAC	180
	:::	
Db	41	
Db	GLIYLSALARPOLYSLREULENILETRYALAAIASERTHLEUGINSERCILYVALPROSER	60
Oy	CGATTTCAGTGGCAGCGGGTCTGGGACAAATTTCACTCTCAGTACAGCATGCTTCACACT	240
	:::	
Db	61	
Db	ARSPHESEIRLYSERGISYSEIRGLYTHRAPHERLIEUTHRIEASISSEIENGLNPRO	80
Oy	GAGATCTTCACACTTACTGTCCAGACAGATCGACATCCCGCTACACTTTTGGCCAG	300
	:::	
Db	81	
Db	GLIUSPHEHALIATHIRYTRYCYSGLINGIINTRAENSERPHENOLEUTHRPHEOGLYLY	100
Oy	GGGACCAAGCTGGAGATCAAA	321
	:::	
Db	101	
Db	GLIYTHIRYLSLEUGIUIIEIYLS	107

## RESULT 13

S31980

Ig kappa chain - human (Fragment)  
C; Species: Homo sapiens (man)

C:\Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:\Accession: S31980; S32000

R. Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McIachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992

A: Description: Lack of promiscuity in autotransgen-specific H and L chain combinations as demonstrated by the *anti*-*data* experiment, June 1997

A;Accession: S31980

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <POR>

A/Cross-references: EMBL:Z15076; NID:g38491; PIDD:CAA18785.1; PID:g38492; EMBL:Z15083; NID:g38491; PIDD:CAA18785.1; PID:g38492

C/Superfamily: immunoglobulin V region; immunoglobulin homology

**C/Keywords:** heterotetramer; immunoglobulin F16-90/Domain: immunoglobulin homology <Imm>

Alignment Scores:

### Alignment Scores:

Pred. No.:	2.99e-32	Length:	100
Score:	441.00	Matches:	85
Percent Similarity:	86.92%	Conservative:	8
Best Local Similarity:	79.44%	Mismatches:	14
Query Match:	77.23%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-141 (1-321) X S31980 (1-109)

Oy	1	GAGCTCCAGATGACCCAGTCTCCATCTCTCTGTCTGTTCTGTGGGAGACAGATCAC	60
Db	1	GlutueValmetThrInserProSerSerLeuSerAlaSerValGlyAspIryValThr	20
Oy	61	ATCATCTGTGGACAGCACTCAGACATTAGCAGCTATTAAATTGGTATCAGCAAAACCA	120
Db	21	IleSerCysArgAlaSerGlnMetIleGlyIyValTyLeuAsnTriPyArgIlnIysPro	40
Oy	121	GGACAGCCTCCTTAAGCTGCTCATTTACTGGCCATCTACCCGGGAATCCGGGATCCCTTAC	180
Db	41	GlyIysAlaProGlnLeuLeuIleIyGlyThrSerThrLeuGlnIserGlyValProSer	60
Oy	181	CGATTTCATGGCAGCGGCTCTGGGACAGATTTCATCTCAATATCAGCATGTCTTAACCT	240

Db	6	ArgPheSerCylserGlyPheGlyThrNapheTrileuTrilleSerSerLeuGlnPro	80
Qy	241	GAAGATTCTGCACCTACTACTGTGAGAGATTACGACATCCGTCACATTTTGGCAG	3000
Db	81	GlnaPhePhealThrTyrrPheCysGlnGlninsertYrrSerSerProTyrrThrPheGlyGln	1000
Qy	301	GGGACCAAGCTGGAGATCAA	321
Db	101	GlyThrIysLeuGlnIleGln	107

**RESULT 14**

S46370

Ig kappa chain V-J region (T23-9) - human (fragment)  
 C:Species: Homo sapiens (man)

C:/Accession: S46370; S38644  
C:/date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #next\_change 21-Jan-2000

R. Bensimon, C.; Chastagner, P.; Zouali, M.  
EMBO J. 13, 2951-2962, 1994

A, Title: Human lupus anti-DNA autoantibodies undergo es  
A, Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46370  
A:Molecule type: mR

A;Residues: 1-120 <BEN>

**A;Cross-references: EMB**

C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

F;26-100/Domain: Immunoglobulin homology <IMM>

Alignment Scores: 5.53e-32  
Pred. No.: Length:

### Alignment Scores:

Pred. No.:	5.53e-32	length:	12
Score:	438.00	Matches:	87
Percent Similarity:	87.96%	Conservative:	8
Best Local Similarity:	80.56%	Mismatches:	11
Query Match:	76.71%	Indels:	2
DB:	2	Gaps:	1

US-09-403-107-141 (1-321) X S46370 (1-120)

```

QY      1 GAGCTCCAGATGATGACCCAGTCTCCATCTCTCCCTGTCTGCTTCTGGAGACAGAGTCAAC 60
      .....
Db      11 AsplIeGImeThrGlnSerProSerSerIeSerValGlyAspArgValThr 30
      .....
QY      61 ATCACTGTCGACAGTCAAGCATTTAGCAGCATTAATAATGGATTCACGACAGAAACA 120
      .....
Db      31 IletmCYsArgAlaSerArgSerIleSerSerPheLeuSerIlePyrGlnGlnysPro 50
      .....
QY      121 GGACAGCCCTCCATGCTGCTCAATTTACTGCGCATTAACCCGGAATCCGGGCTCCAGC 180
      .....
Db      51 GlyIysAlaProGlnLeuLeuIleTyrAlaValSerArgLeuGlnSerGlyValProSer 70
      .....
QY      181 CGATTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTTCAACCATCAGACGTCTACACCT 240
      .....
Db      71 ArgPheSerGlySerGlyIleSerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 90
      .....
QY      241 GAAGATTCTCGCAACTACTACTCTGACGAGATAGCAACATCCCG-----TACACTTT 294
      .....
Db      91 GluAspPheAlaThrTyrTyrCysGlnGlnSerPheSerAsnProGlnIleTyrThrPhe 110
      .....
QY      295 GGCCAGGGGACCAAGCTGGAGATC 318
      .....
Db      111 GlyGlnGlyThrIleLeuGlnIle 118

RESULT 15
S31977
Ig kappa chain - human
C.Species: Homo sapiens (man)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C.Accession: S31977
R.Portolano, S.; Chazenbalk, G.D.; Hutchinson, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A.Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A.Reference number: S31977
A.Accession: S31977

```



A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <PDR>  
 C:Cross-references: UNIPROT:Q96SA9, EMBL:Z15073  
 C:Superfamily: immunoglobulin V region, immunoglobulin homology  
 C:Keywords: heterotetramer, immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IM>

Alignment Scores:  
 Pred. No.: 6,92e-32 Length: 108  
 Score: 437.00 Matches: 87  
 Percent Similarity: 86.92% Conservative: 6  
 Best Local Similarity: 81.31% Mismatches: 14  
 Query Match: 76.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-403-107-141 (1-321) x S31977 (1-108)

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QY 1 GAGCTCCAGATGATGACCCAGTCTCCATCTCCCTGCTGCTGTTGTTGGAGACAGATCACC 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1 GlnLeuValMetThrGlnSerGlySerSerLeuSerAlaSerValGlyAspArgValThr 20

QY 61 ATCACTTGTCCGACAAAGTCAGACATTAAGCACTTAATAATTGGTATCAGCAGAAACCA 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 21 IleThrCysArgAlaSerGlnSerIleSerAlaTyrLeuAsnTrpTyrGlnIleValysPro 40

QY 121 GGACAGCCTCCTTACCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 41 GlyValAlaProLysLeuLeuIleTyrSerAlaSerSerLeuGlnSerGlyValProSer 60

QY 181 CGATTCAAGTGCAGCGGGGCTTGGACAGATTCACTTCACCATCAGCAGATCTACAACCT 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 61 ArgPheSerGlySerGlySerGlyThrAspPheMetLeuThrIleSerSerLeuGlnPro 80

QY 241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTAGACATCCCGTACACTTTTGGCCAG 300
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 81 GlnAspPheAlaThrTyrTyrCysGlnGlnSerTyrAspThrValAspThrPheGlyHis 100

QY 301 GGGACCAAGCTGGAGATCAA 321
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 101 GlyThrLysValGlnIleLys 107
  
```

Search completed: August 29, 2005, 11:31:14  
 Job time : 16.4038 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_nzp model

Run on: August 29, 2005, 11:01:36 ; Search time 68.3611 Seconds  
(without alignments)  
4809.091 Million cell updates/sec

Title: US-09-403-107-141  
Perfect score: 571  
Sequence: 1 gagctccagatgaccagtc.....ggaccagctcgagatcaaa 321

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Command line parameters:

-MODEL=frame\_nzp\_model -DEV=xlp  
-O=/cgn2.1/USPRO\_epool\_p/US09403107/runat\_29082005\_120124\_18889/app\_query.fasta\_1.1038  
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09403107@cgn\_1\_1\_305@runat\_29082005\_120124\_18889 -NCPU=6 -ICPU=3  
-NO MAP -LARGESQUERY -NEG SCORES=0 -WAIT -DISPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_03.\*

1: uniProt\_sprot.\*  
2: uniProt\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	79.2	108	Q9UL77	Q9UL77 homo sapien
2	450	78.8	129	KV1V_HUMAN	P0431 homo sapien
3	440.5	77.1	107	Q96SA9	Q96SA9 homo sapien
4	436	76.4	108	KV1J_HUMAN	P01600 homo sapien
5	435	76.2	134	KV4C_HUMAN	P06314 homo sapien
6	434	76.0	114	KV4A_HUMAN	P01625 homo sapien
7	433	75.8	108	KV1I_HUMAN	P01605 homo sapien
8	433	75.8	236	O6GMX1	O6GMX1 homo sapien
9	433	75.8	236	O6GMX8	O6GMX8 homo sapien
10	431	75.5	236	O6GMX0	O6GMX0 homo sapien
11	424	74.3	108	KV1E_HUMAN	P01597 homo sapien
12	424	74.3	108	Q9UL70	Q9UL70 homo sapien
13	422	73.9	108	KV1O_HUMAN	P01607 homo sapien
14	421	73.7	108	KV1J_HUMAN	P01594 homo sapien
15	420	73.6	108	KV1N_HUMAN	P01606 homo sapien
16	420	73.6	108	KV1Y_HUMAN	P00362 homo sapien

17	420	73.6	236	2	O6P1T5	O6P1T5 homo sapien
18	415.5	72.8	107	2	Q9UL81	Q9UL81 homo sapien
19	414	72.5	236	2	O6P1H7	O6P1H7 homo sapien
20	413	72.3	108	1	KV1V_HUMAN	P0430 homo sapien
21	412	72.2	108	1	KV1K_HUMAN	P01603 homo sapien
22	412	72.2	234	2	Q7Z473	Q7Z473 homo sapien
23	412	72.2	236	2	O7Z3Y4	O7Z3Y4 homo sapien
24	411	72.0	108	1	KV1P_HUMAN	P01608 homo sapien
25	411	72.0	108	2	Q9UL79	Q9UL79 homo sapien
26	407	71.3	108	1	KV1Q_HUMAN	P01604 homo sapien
27	406	71.1	108	1	KV1L_HUMAN	P01604 homo sapien
28	405.5	71.0	133	1	KV4B_HUMAN	P06313 homo sapien
29	404	70.8	108	1	KV1A_HUMAN	P01593 homo sapien
30	404	70.8	108	1	KV1S_HUMAN	P01611 homo sapien
31	403.5	70.7	107	1	KV1D_HUMAN	P01596 homo sapien
32	402	70.4	108	1	KV1C_HUMAN	P01595 homo sapien
33	401	70.2	108	1	KV1R_HUMAN	P01610 homo sapien
34	401	70.2	108	1	KV1P_MOUSE	P01649 mus musculus
35	398	69.7	244	2	O6S2C8	O6S2C8 homo sapien
36	397	69.5	108	1	KV1P_HUMAN	P01598 homo sapien
37	394	69.0	236	2	O6GMX9	O6GMX9 homo sapien
38	394	69.0	240	2	O6S2C9	O6S2C9 homo sapien
39	392	68.7	129	1	KV1X_HUMAN	P04432 homo sapien
40	391.5	68.6	109	1	KV1T_HUMAN	P01612 homo sapien
41	391	68.5	108	1	KV1G_HUMAN	P01599 homo sapien
42	391	68.5	108	1	KV5M_MOUSE	P01646 mus musculus
43	388	68.0	109	1	KV4D_HUMAN	P03593 homo sapien
44	388	68.0	111	2	Q920B9	Q920B9 mus musculus
45	386	67.6	111	1	KV3M_MOUSE	P01665 mus musculus

#### ALIGNMENTS

RESULT 1  
ID Q9UL77 PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000 (Trembl, 13, Created)  
DT 01-MAY-2000 (Trembl, 13, Last sequence update)  
DT 01-OCT-2003 (Trembl, 25, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56273.1; --  
DR PIR; B49047; B49047.  
DR HSSP; P01607; IBMW.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1\_v.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;  
Alignment Scores:  
Pred. No.: 7.19e-40 Length: 108  
Score: 452.00 Matches: 87  
Percent Similarity: 88.79% Conservative: 8  
Best Local Similarity: 81.31% Mismatches: 12  
Query Match: 79.16% Indels: 0  
DB: Gaps: 0

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US-09-403-107-141 (1-321) x Q9UL77 (1-108)
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 60
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 61 ATCACTTGTGGACAAGTCAGACATTAGACGATTAATAATGGTATCGACGAACA 120
Db 21 ILeThrCyArgAlaSerGlnSerIleSerSerThrLeuGlnTrpGlnGlnlySpro 40
QY 121 GACAGCCTTCAGTCTGCTCATTTACTGCGCATCAACCGGGAATCCGGGGTCCCTGAC 180
Db 41 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
QY 181 CGATTTCAGTGGACGGGGTCTGGACAGATTTTCACTTCACCATTCAGACGTCACACT 240
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 241 GAAGATTCTGCACACTTACTCTGTCAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrSerTrpThrPheGlyGlu 100
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 101 GlyThrLysValGluIleLys 107
RESULT 2
KV1W_HUMAN STANDARD; PRT; 129 AA.
ID KV1W_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15-kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Kloback H.G., Combracio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUMK.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003623; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 129 Ig kappa chain V-I region Walker.
FT SIGNAL 22
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
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FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; P941FA07DA4FC2F9 CRC64;

Alignment Scores:
Pred. No.: 129
Score: 450.00 Length: 129
Percent Similarity: 88.79% Matches: 88
Best Local Similarity: 82.24% Mismatches: 12
Query Match: 78.81% Indels: 0
DB: 1 Gaps: 0

US-09-403-107-141 (1-321) x KV1W_HUMAN (1-129)
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCCTGCTTCTGTGGAGACAGAGTCACC 60
Db 23 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 42
QY 61 ATCACTTGTGGACAAGTCAGACATTAGACGATTAATAATGGTATCGACGAACA 120
Db 43 ILeThrCyArgAlaSerGlnSerIleSerSerThrLeuGlnTrpGlnGlnlySpro 62
QY 121 GACAGCCTTCAGTCTGCTCATTTACTGCGCATCAACCGGGAATCCGGGGTCCCTGAC 180
Db 63 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValThrSer 82
QY 181 CGATTTCAGTGGACGGGGTCTGGACAGATTTTCACTTCACCATTCAGACGTCACACT 240
Db 83 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 102
QY 241 GAAGATTCTGCACACTTACTCTGTCAGACAGATTTCAGACATCCCGTACACTTTGGCCAG 300
Db 103 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrLeuIleThrPheGlyGlu 122
QY 301 GGGACCAAGCTGGAGATCAAA 321
Db 123 GlyThrArgLeuGlnIleLys 129
RESULT 3
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain
DE variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mysin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
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DR PROSITE, PSS0835; IG LIKE; 1.  
FT NON TER 1  
FT NON TER 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;  
Alignment Scores:  
Pred. No.: 1,25e-38 Length: 107  
Score: 440.50 Matches: 88  
Percent Similarity: 87.85% Conservative: 6  
Best Local Similarity: 82.24% Mismatches: 12  
Query Match: 77.15% Indels: 1  
DB: 2 Gaps: 1  
US-09-403-107-141 (1-321) x Q96SA9 (1-107)  
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCTGCTGCTTGCGGAGACAGATCACC 60  
Db 1 AsplieglnmetrhglnserproserSerleuSerValIGlyAspArgValThr 20  
QY 61 ATCACTGTGCGACAGTACGAGCTTAGCAGCTATTAATAATGGTATCAGAGAAACA 120  
Db 21 ILehrCySaRgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnPro 40  
QY 121 GGACAGCCTCTAGCTGCTCATTTACTGCGAGTACCCGGGAATCCGGGTCCTGAC 180  
Db 41 GlySaAlaProGlnLeuLeuLeuLeuTyAlaAlaSerSerleuGlnSerGlyValProser 60  
QY 181 CGATTCAAGTGGCAGCGGGGTCTGGAGACAGATTCTCACTTCACCATAGAGATCTCAACCT 240  
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerleuGlnPro 80  
QY 241 GAAGTTCTGCAACTTACTCTACGTCAGAGCTTACGACATCCCTACACTTTGGCCAG 300  
Db 81 GluAspPheAlaThrTyTyTyGlnGlnSerTySer--ThrLeuThrPheGlyGln 99  
QY 301 GGACCAAGCTGGAGATCAAA 321  
Db 100 GlyThrTyValGlnIleGly 106  
RESULT 4  
KV1H\_HUMAN STANDARD; PRT; 108 AA.  
ID KV1H\_HUMAN STANDARD; PRT; 108 AA.  
AC P01600;  
DT 21-JUN-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE IG kappa chain V-I region Hau.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OC NCB1\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within RT subgroups.";  
RL Hoppe-Sejler S Z. Physiol. Chem. 351:1291-1295 (1970).  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
DR PIR, A01868; K1H0HU.  
DR PDB, 1F6L; X-ray; L=1-108.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig, 1.  
DR SMART; SM00406; IGV, 1.  
DR PROSITE; PSS0835; IG LIKE; 1.  
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 34 Complementarity-determining-1.  
FT DOMAIN 35 49 Framework-2.  
FT DOMAIN 50 56 Complementarity-determining-2.  
FT DOMAIN 57 88 Framework-3.  
FT DOMAIN 89 97 Complementarity-determining-3.  
FT DOMAIN 98 107 Framework-4.  
FT DISUPD 23 88 By similarity.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;  
Alignment Scores:  
Pred. No.: 3,83e-38 Length: 108  
Score: 436.00 Matches: 84  
Percent Similarity: 88.79% Conservative: 11  
Best Local Similarity: 78.50% Mismatches: 12  
Query Match: 76.36% Indels: 0  
DB: 1 Gaps: 0  
US-09-403-107-141 (1-321) x KV1H\_HUMAN (1-108)  
QY 1 GAGCTCCAGATGACCCAGTCTCCATCTCCTGCTGCTTGCGGAGACAGATCACC 60  
Db 1 AsplieglnmetrhglnserproserSerleuSerValIGlyAspArgValThr 20  
QY 61 ATCACTGTGCGACAGTACGAGCTTAGCAGCTATTAATAATGGTATCAGAGAAACA 120  
Db 21 ILehrCySaRgAlaSerGlnSerIleSerSerTyLeuAsnTrpTyGlnGlnPro 40  
QY 121 GGACAGCCTCTAGCTGCTCATTTACTGCGAGTACCCGGGAATCCGGGTCCTGAC 180  
Db 41 GlySaAlaProGlnValLeuLeuLeuTyAlaAlaSerSerleuProserGlyValProser 60  
QY 181 CGATTCAAGTGGCAGCGGGGTCTGGAGACAGATTCTCACTTCACCATAGAGATCTCAACCT 240  
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerleuGlnPro 80  
QY 241 GAAGTTCTGCAACTTACTCTACGTCAGAGCTTACGACATCCCTACACTTTGGCCAG 300  
Db 81 GluAspPheAlaThrTyTyTyGlnGlnSerTySerIleThrProThrSerPheGlyGln 100  
QY 301 GGACCAAGCTGGAGATCAAA 321  
Db 101 GlyThrArgValGlnIleGly 107  
RESULT 5  
KV4C\_HUMAN STANDARD; PRT; 134 AA.  
ID KV4C\_HUMAN STANDARD; PRT; 134 AA.  
AC P06314;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-APR-1988 (Rel. 07, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG kappa chain V-IV region B17 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OC NCB1\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86041854; PubMed=2997713;  
RA Marsh P., Mills F., Gould H.;  
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA RT probe.";  
RL Nucleic Acids Res. 13:6531-6544 (1985).  
RN [2]  
RP REVISION TO 76.  
RA Marsh P.;  
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.  
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QY 1 GAGCTCCAGATGACCCAGATCTCCATCTCCGTCGTCCTTCTGCGGAGACAGATCAC 60
Db 1 AsplilevalmetrthinserserproaspserleuAlaValSerleuGlyGlntrgAlaThr 20
QY 61 ATCACTTGTGCGACAGATGACGACAT-----AGCAGCTATTAAAT 102
Db 21 IleAncylyserSerSerleuValleuTyrserserAasnSerlyAsnlyrleuAla 40
QY 103 TGGTATCAGCAGAAACAGAGACAGCTCTTAAGCTGCTCATTTACTGGCGATTCACCGG 162
Db 41 TPTTYTGInGlnLysProGlyGlnProProlYsleuLeuIleTyrtPAlaserThrArg 60
QY 163 GAATCCGGGGTCCCTGACCGGATTCAGTGGCAGCGGGTCTGGAGCAGATTTCACCTCAC 222
Db 61 GlusertGlyValProaspPsrpheserGlyserGlyThrAspPheThrleuThr 80
QY 223 ATCAGCAGCTTCAACACTGAGATTCCTGCACTTACTACTGTACAGCAGAGTTCAGACATC 282
Db 81 IleserSerleuGlnAlaGlnuapValAlaValTyrtYrCyseGlnGlnTyrtYrserThr 100
QY 283 CCGTACACTTGGCCGACGGGACCAAGCTGAGATCAAA 321
Db 101 ProTyserPheGlyGlnGlyThrlyserGlnIlelys 113

RESULT 7
KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-1 region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IGM
RT anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: The second and third hypervariable regions of this
CC chain are identical with those of the human POM V-III kappa chain,
CC with which it shares certain idiotypic determinants.
CC -I- MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma
CC globulin activity.
CC PIR: A01871; KIHULY.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

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Alignment Scores: 8.07e-38 Length: 108  
 Pred. No.: 433.00 Matches: 82  
 Score:

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Percent Similarity: 86.92% Conservative: 11
Best Local Similarity: 76.64% Mismatches: 14
Query Match: 75.83% Gaps: 0
DB: 1 Indels: 0

US-09-403-107-141 (1-321) x KVLM_HUMAN (1-108)
QY 1 GAGCTCCAGATGACCCAGATCTCCATCTCCGTCGTCCTTCTGCGGAGACAGATCAC 60
Db 1 AsplilegmetrthinserserproaspserleuAlaValSerleuGlyGlntrgAlaThr 20
QY 61 ATCACTTGTGCGACAGATGACGACATTTAAATTTGGTTCACAGAAACCA 120
Db 21 IletnrcysglnAlaSerGlnAsnValAsnAlaTyrtYrleuAsntrPyrGlnLysPro 40
QY 121 GGACAGCCTCTTAAGCTGCTCATTTACTGGCGATTCACCGGGAATCCGGGGTCCCTGAC 180
Db 41 GlyleuAlaProlYsleuLeuIleTyrclyAlaserThrArgGlnAlaGlyValPsrser 60
QY 181 CGATTTCAGTGGCAGCGGGTCTGGAGCAGATTTCACCTCACAGCAGTTCACAACT 240
Db 61 ArgPheSerGlyserGlyserGlyThrAspPheThrIleSerSerleuGlnPro 80
QY 241 GAAGATCTCGCACTTACTACTGTACAGAGATTCACCGGATCACTTGGGCGAG 300
Db 81 GlusplleAlaIleAlaTyrtYrCyseGlnGlnTyrtYrAsnAsntrProlProtnPheGlyGln 100
QY 301 GGACCAAGCTGAGATCAAA 321
Db 101 GlyThrlyserValGlnVallys 107

RESULT 8
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
ID Q6GMW1;
DT 05-JUL-2004 (TREMBLRel. 27, Created)
DT 05-JUL-2004 (TREMBLRel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLRel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadler M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huliy R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalela U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC073791; AAH73791.1; -.

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Db      41 GlyLeuAlaProlyValLeuIlePheAlaAlaSerSerLeuYsSerGlyValProSer 60
Qy      181 CGATTGAGTGGCAGCGGGTCTGGGACGAGATTTCACTCTCCATCAGAGACTTACAACT 240
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerGlyLeuPro 80
Qy      241 GAAGATTCTCGACACTTACTACTGTCAGACAGATTACGACATCCCGTACACTTTGGCCAG 300
Db      81 GluAspPheAlaThrTrpTrpCysGlnGlnSerTrpThrProTrpThrPheGlyPro 100
Qy      301 GGGACCAAGCTGGAGATC 318
Db      101 GlyThrValGluMet 106

RESULT 12
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; IBMW.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Alignment Scores:
Pred. No.: 7.55e-37 Length: 108
Score: 424.00 Matches: 84
Percent Similarity: 84.11% Conservative: 6
Best Local Similarity: 78.50% Mismatches: 17
Query Match: 74.26% Indels: 0
DB: 2 Gaps: 0

US-09-403-107-141 (1-321) x Q9UL70 (1-108)
Qy      1 GAGGTCCAGATGAGCCAGTCCATCTCCCTGCTGCTTCTGTGGGAGACAGAGTACC 60
Db      1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
Qy      61 ATCACTGTGCGACACTGTCAGACAGACTTACGACTATTAATTGGTATCAGCAAAACA 120
Db      21 IleThrYsArgAlaSerGlnGlyIleSerAsnTyrIleuAlaTrpTrpGlnGlnYsPro 40
Qy      121 GAGACGCTCTTAAGCTGCTCATTTACTGGCGATTAACCCGGGAGATCCGGGGTCCCTGAC 180
Db      41 GlyValValProYsSerLeuIleTyrAlaAlaSerThrIleuGlnSerGlyValProSer 60
Qy      181 CGATTGAGTGGCAGCGGGTCTGGGACGAGATTTCACTCTCCATCAGAGACTTACAACT 240
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrIleuThrIleSerSerLeuGlnPro 80
Qy      241 GAAGATTCTCGACACTTACTACTGTCAGACAGATTACGACATCCCGTACACTTTGGCCAG 300

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Db      81 GluAspValAlaThrTrpTrpCysGlnYsTyrAsnSerAlaProArgThrPheGlyPro 100
Qy      301 GGGACCAAGCTGGAGATCAA 321
Db      101 GlyThrValLeuGlnIleLeys 107

RESULT 13
KV10_HUMAN STANDARD; PRT; 108 AA.
ID KV10_HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Rel.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein: a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Bpp O., Latzman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1 MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1 MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A9163; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BW; X-ray; A/B=1-107.
DR PDB; 1RE1; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006953; F:immune response; NAS.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57

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QY 241 GAAGATTCGCAACTTACTGTGTCAGAGATTACGATCCCGTACCTTTTGGCCAG 300
    |||||
Db 81 GUAAspIleAlaThrTrpTyrCysGlnGlnTyrAspTyrLeuProThrPheGlyGln 100
    |||||
QY 301 GGGACCAAGCTGGAGATCAAA 321
    |||||
Db 101 GlyThrLysValGluIleLys 107
    |||||

RESULT 15
KV1N_HUMAN STANDARD; PRT; 108 AA.
ID KV1N_HUMAN
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE 1g kappa chain V-1 region OV.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
DR HSP: A01872; KIHUO.
DR HSP: P01607; IBMW.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS00835; Ig_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105827E CRC64;

Alignment Scores:
Pred. No.: 2.04e-36 Length: 108
Score: 420.00 Matches: 73
Percent Similarity: 85.98% Conservative: 19
Best Local Similarity: 68.22% Mismatches: 15
Query Match: 73.56% Indels: 0
DB: Gaps: 0

US-09-403-107-141 (1-321) x KV1N_HUMAN (1-108)
QY 1 GAAGCTCAGATGAGCCAGTTCATCTCCGTGTCGTGTCGGAGACAGAGTCACC 60
    :
Db 1 AspIleGlnMetThr**SerProSerSerLeuSerAlaSerValGly**ArgValThr 20
    :

QY 61 ATCACTTGTGCAAGTCAAGTTCAGCATTTAGCAGTATTAATGTATCAGCAAAACA 120
    |||||
Db 21 IleThrCysArgAlaSer**ThrIleSerSerTyrLeu**TrpTyr*****LysPro 40
    |||||

QY 121 GACAGAGCTCTTAAGTCTCATTTACTGGCATCTACCCGGGAATCCGGGCTCCTGAC 180
    |||||
Db 41 GlyLysAlaPro**LeuLeuIleTyrAlaAlaSer**LeuHisSerGlyValProSer 60
    |||||
```

```
QY 181 CGATTGAGTGGAGGGGTCTGGGACAGATTTCACTTCACCATGAGGATCTACACCT 240
    |||||
Db 61 ArgPheSerGlySerGlySerLeuThr**PheThrPheThrIleSerSerLeu**Pro 80
    |||||

QY 241 GAAGATTCGCAACTTACTGTGTCAGAGATTACGATCCCGTACCTTTTGGCCAG 300
    |||||
Db 81 *****PheAlaThrTyrTyrCys*****SerTyrSerSerProThrThrPheGly*** 100
    |||||

QY 301 GGGACCAAGCTGGAGATCAAA 321
    |||||
Db 101 GlyThrArgLeu**IleLys 107
    |||||
```

Search completed: August 29, 2005, 11:06:45  
Job time : 71.3611 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 95.5214 Seconds  
(without alignments)  
3085.293 Million cell updates/sec

Title: US-09-403-107-143\_COPY\_1\_381  
Perfect score: 696  
Sequence: 1 gaggtgcagctgcgcagtc.....ccacgctccacctctctcca 381

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p model -DEV=x1p  
-O=/cgn2.1/USPRO\_EPROT\_P/US09403107/runat\_29082005\_120124\_18882/bpp\_query.fasta\_1.1038  
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=humand0.cdi -LIST=45  
-DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=apco -NORM=ext -HEAPSIZE=500 -MINLEN=200000000  
-USER=US09403107 @CGN\_1\_1\_308 @runat\_29082005\_120124\_18882 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGOQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1980s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686	98.6	127	2	AAV17954 Human D4.
2	686	98.6	138	2	AAW80815 Amino aci
3	686	98.6	523	3	AAV44994 HD70scFv-
4	686	98.6	524	3	AAV44995 HD70scFv-
5	608.5	87.4	124	6	ADA89238 Human ant
6	598.5	86.0	122	8	ADK38663 Mouse hea
7	597.5	85.8	122	8	ADP22128 Human ant
8	597.5	85.8	122	8	ADK38664 Mouse hea
9	595.5	85.6	126	8	ADP22222 Human ant
10	594.5	85.4	143	3	AAV82629 Human PTH

11	591	84.9	451	3	AAV93734 The heavy
12	591	84.9	451	6	AAE35689 Human 11.
13	590	84.8	123	8	ADK84396 Human ant
14	590	84.8	123	8	ADK68538 Anti-EPO-
15	589.5	84.7	118	5	AAV51167 Human DP-
16	589.5	84.7	126	7	ADK18786 Anti-huma
17	589.5	84.7	126	7	ADK18822 Anti-huma
18	589.5	84.7	126	7	ADK18882 Anti-huma
19	589.5	84.7	126	7	ADK18593 Anti-huma
20	589.5	84.7	126	7	ADK18785 Anti-huma
21	589.5	84.7	126	7	ADK18601 Anti-huma
22	589.5	84.7	126	7	ADK18858 Anti-huma
23	589.5	84.7	126	8	ADL25404 Human mab
24	589.5	84.7	126	8	ADL25420 Human mab
25	589.5	84.7	134	8	ADP22348 Human ant
26	589	84.6	146	5	AAV51169 Human rec
27	588.5	84.6	143	3	AAV82621 Human PTH
28	588	84.5	146	5	AAV51172 Human rec
29	587.5	84.4	143	3	AAV82625 Human PTH
30	587	84.3	123	8	ADK84372 Human ant
31	587	84.3	123	8	ADK68514 Anti-EPO-
32	586.5	84.3	143	3	AAV82622 Human PTH
33	586.5	84.3	143	3	AAV82623 Human PTH
34	586	84.2	123	8	ADP22218 Human ant
35	586	84.2	146	5	AAV51171 Human rec
36	586	84.2	146	5	AAV51168 Human rec
37	586	84.2	252	5	ADP45720 Human Bly
38	586	84.2	252	7	ADG96547 Single ch
39	585.5	84.1	249	5	ADP44501 Human Bly
40	585.5	84.1	249	5	ADG95328 Single ch
41	584.5	84.0	249	5	ADP45091 Human Bly
42	584.5	84.0	249	5	ADP45104 Human Bly
43	584.5	84.0	249	5	ADP44386 Human Bly
44	584.5	84.0	249	5	ADG95213 Single ch
45	584.5	84.0	249	7	ADG95918 Single ch

## ALIGNMENTS

RESULT 1	AAV17954 standard; protein; 127 AA.
AAV17954	
XX	
AC	AAV17954;
XX	
DT	04-AUG-1999 (first entry)
XX	
DE	Human D4.5 heavy chain variable region.
XX	
KW	Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW	autoimmune disease; scFv-antibody; single-chain Fv.
XX	
OS	Homo sapiens.
XX	
PN	W09925818-A1.
XX	
PD	27-MAY-1999.
XX	
PF	16-NOV-1998; 98WO-EP007313.
XX	
PR	17-NOV-1997; 97EP-00120096.
XX	
PA	(KUFE/) KUFER P.
XX	
PI	Kufner P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX	
DR	WPI: 1998-338004/28.
XX	
NR	N-PSDB; AAX77236.
XX	
PT	Phage display system for identification of binding site domains retaining
XX	capacity to bind an epitope.
XX	
PS	Disclosure; Fig 3.1; 152pp; English.

XX The invention relates to a method of identifying binding site domains  
CC (BSD) that retain the capacity of binding to a predetermined epitope when  
CC positioned C-terminal of at least one further domain in a recombinant bi-  
CC or multivalent polypeptide. The method comprises (a) testing a panel of  
CC BSD displayed on the surface of a biological display system as part of a  
CC fusion protein for binding to a predetermined epitope, where the fusion  
CC protein comprises an additional domain positioned N-terminal of the BSD  
CC and an amino acid sequence that mediates anchoring of the fusion protein  
CC to the surface of the display system; and (b) identifying a BSD that  
CC binds to the predetermined epitope. The method is useful to identify bi-  
CC or multivalent polypeptides that comprise antibody binding sites capable  
CC of efficiently binding to the corresponding antigen. The polypeptides or  
CC antibodies identified by the method are useful therapeutically and  
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody  
CC fragments that bind independently of their position within bifunctional  
CC single-chain fusion proteins can be isolated from combinatorial antibody  
CC libraries using the new in vitro method

XX Sequence 127 AA:

SQ

## Alignment Scores:

Pred. No.:	1.08e-62	Length:	127
Score:	686.00	Matches:	126
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.21%	Mismatches:	0
Query Match:	98.56%	Indels:	0
DB:	2	Gaps:	0

US-09-403-107-143\_COPY\_1\_381 (1-381) x AAM17954 (1-127)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGCGCTGCTCCAGGAGTCCCTGAGACTC 60  
DB 1 GluValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCTGTGACAGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGAGCTCCGACAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40  
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGCGATTATATCATATGATGAGTAATAATACTAT 180  
DB 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60  
QY 181 GCAGACTCCGCTGAAGGGCCGATTTCACATCTCCAGAGACAATTCAGAGACAGCTGTAT 240  
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80  
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAAGATATG 300  
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAspMet 100  
QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATATGACGTCGGGGCCAAAGG 360  
DB 101 GlyTrpGlySerGlyTrpArgProTyrTyrTyrTyrGlyMetAspValTrpGlyGlnGly 120  
QY 361 ACCACGGTCAACCGTCTCTCA 381  
DB 121 ThrThrValThrValSerSer 127

## RESULT 2

AAM80815 ID AAM80815 standard; protein; 138 AA.

AC AAM80815;

DT 16-FEB-1999 (first entry)

DE Amino acid sequence of human D4.5 heavy chain variable region.

XX Human; D4.5 heavy chain variable region; receptor; antigen; tumour;  
KM auto-immune disease; graft rejection; allergy; inflammatory disease;  
KM endocrine disease; degenerative disease.

OS Homo sapiens.

XX WO9846645-A2.

XX 22-OCT-1998.

XX 14-APR-1998; 98MO-EP002180.

XX 14-APR-1997; 97EP-00106109.

XX (KUPE/) KUPE P.

XX (RAUM/) RAUM T.

XX Kufer P, Raum T;

XX WPI; 1998-594564/50.

XX N-PSDB; AAV68537.

XX Production of anti-human antigen receptors - by selecting a combination

XX of functionally rearranged VH and VL immunoglobulin chains expressed from

XX a recombinant vector.

XX Claim 9; Fig 7; 84pp; English.

XX This is the amino acid sequence of the human D4.5 heavy chain variable

XX region, used in the method of the invention, for providing receptors that

XX can be used for targeting antigens in humans without being immunogenic

XX themselves. Such receptors can be used for treating diseases such as

XX tumours or auto-immune diseases, graft rejection after transplantation,

XX infectious diseases by targeting cellular receptors as well as allergic,

XX inflammatory, endocrine and degenerative diseases by targeting key

XX molecules involved in the pathological process

XX Sequence 138 AA:

SQ

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGCGCTGCTCCAGGAGTCCCTGAGACTC 60  
DB 1 GluValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCTGTGACAGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGAGCTCCGACAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40  
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGCGATTATATCATATGATGAGTAATAATACTAT 180  
DB 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60  
QY 181 GCAGACTCCGCTGAAGGGCCGATTTCACATCTCCAGAGACAATTCAGAGACAGCTGTAT 240  
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80  
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAAGATATG 300  
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAspMet 100  
QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATATGACGTCGGGGCCAAAGG 360  
DB 101 GlyTrpGlySerGlyTrpArgProTyrTyrTyrTyrGlyMetAspValTrpGlyGlnGly 120  
QY 361 ACCACGGTCAACCGTCTCTCA 381  
DB 121 ThrThrValThrValSerSer 127

RESULT 3  
 ID AAY44994 standard; protein; 523 AA.  
 AC AAY44994;  
 DT 23-MAY-2000 (first entry)  
 XX  
 XX HD70scFv-CH1-GM-CSF chain.  
 DE  
 KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpcAM;  
 KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;  
 KW granulocyte/macrophage colony stimulating factor; heteromultibody;  
 KW CH1-domain; multifunctional compound; heavy chain constant domain;  
 KW immunoglobulin; cytostatic; immunostimulatory; anti-leukaemia; diagnosis;  
 KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;  
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200006605-A2.  
 XX  
 XX 10-FEB-2000.  
 XX  
 XX 28-JUL-1999; 99WO-EP005416.  
 XX  
 XX 28-JUL-1998; 98EP-00114082.  
 XX  
 XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 XX  
 XX Kufer P, Dreier T, Baueerle PA, Borschert K, Zetl F;  
 PI WPI, 2000-195265/17.  
 DR N-PSDB; AAZ50587.  
 XX  
 XX New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 PT  
 XX  
 XX Example 10; Fig 55A; 166pp; English.  
 XX  
 XX The patent discloses heteromultibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromultibodies have  
 CC cytostatic, immunostimulatory, anti-leukaemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas. The present sequence is the left chain of a  
 CC heteromultibody comprising HD70 single-chain Fv (scFv) fragment N-  
 CC terminally linked to human CH1 domain which bears at its C-terminus the  
 CC human inflammatory cytokine granulocyte/macrophage colony stimulating  
 CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.  
 CC HD70 scFv specifically recognises the human epithelial cell adhesion  
 CC molecule (EpcAM) also called 17-1A antigen  
 XX  
 XX Sequence 523 AA;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,44e-62 Length: 523  
 Score: 686.00 Matches: 126  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.21% Mismatches: 0  
 Query Match: 98.56% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-403-107-143\_COPY\_1\_381 (1-381) x AAY44994 (1-523)

QY 1 GAGGTGCAGCTGCTCGAGTCTGGGGAGAGCCCTGGTCCAGCTGGAGAGTCCCTGAGATC 60  
 Db 142 GIUValGInLeuLeuGInSerGlyGlyValValGInProGlyArgSerLeuArgLeu 161  
 QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTATGAGCATGACCTGGGTCCGACGCT 120  
 Db 162 SerCysAlaAlaSerGlyPheThrPheSerSerGlyGlyMetHisTrpValArgGlnAla 181  
 QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGTAATTAATACTAT 180  
 Db 182 ProGlyLysGlyLeuGInTrpValAlaValIleSerTyrAspGlySerAsnLysTyr 201  
 QY 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCGAGACAAATTCAGACACGCTGAT 240  
 Db 202 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 221  
 QY 241 CTGCAATATGAACACGCTGAGAGTGGAGACACGGCTGTGATTACTGTGCGAAATATG 300  
 Db 222 LeuGlnMetCysSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAspMet 241  
 QY 301 GGGTGGGACAGTGGCTGGAGACCCCTACTACTACTACGATATGACGTCTGGGGCAAAGG 360  
 Db 242 GlyTyrGlySerGlyTyrPargProTyrTyrTyrGlyMetAspValTyrGlyGlnGly 261  
 QY 361 ACCACGGTCAACCTCTCTCTCA 381  
 Db 262 ThrThrValThrValSerSer 268  
 RESULT 4  
 ID AAY44995 standard; protein; 524 AA.  
 AC AAY44995;  
 DT 23-MAY-2000 (first entry)  
 XX  
 XX HD70scFv-CK-interleukin 2.  
 DE  
 KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;  
 KW EpcAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
 KW interleukin-2; CK-domain; kappa light chain constant domain;  
 KW heteromultibody; multifunctional compound; immunoglobulin; cytostatic;  
 KW immunostimulatory; anti-leukaemia; diagnosis; prevention;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200006605-A2.  
 XX  
 XX 10-FEB-2000.  
 XX  
 XX 28-JUL-1999; 99WO-EP005416.  
 XX  
 XX 28-JUL-1998; 98EP-00114082.  
 XX  
 XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
 XX  
 XX Kufer P, Dreier T, Baueerle PA, Borschert K, Zetl F;  
 PI WPI, 2000-195265/17.  
 DR N-PSDB; AAZ50588.  
 XX  
 XX New multifunctional compounds useful for preventing and/or treating  
 PT malignant cell growth and for detection and diagnosis.  
 PT  
 XX  
 XX Example 10; Fig 55B; 166pp; English.  
 XX  
 XX The patent discloses heteromultibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin





Db 41 ProGlyLySGlyLeuGluTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60  
Qy 181 GCAGACTCCGTGAAAGGCGGATTCACCATCTCCAGAGACAAATTCAGAACACGCTGAT 240  
Cc 61 AlaAspSerValLySGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80  
Qy 241 CTGCAAAATGAAGAGCTGAGCTGAGACACGCGCTGCTATTAATCTGCGAAATATG 300  
Db 81 LeuGlnMetAsnSerLeuArgIleValAspThrAlaValTyrCysAlaArgAspPhe 100  
Qy 301 GGGTGGGCGAGTGGCTGAGACCTTACTACTACGATATGAGCTGGGCGCAAGG 360  
Db 101 AspTyrGlyArgSer-----TyrTyrTyrTyrGlyMetAspValTrrpGlyGlnGly 117  
Qy 361 ACCACGGTCACCGCTCTCTCA 381  
Db 118 ThrThrValThrValSerSer 124  
RESULT 6  
ADR38663  
ID ADR38663 standard, peptide, 122 AA.  
XX ADR38663;  
AC 02-DEC-2004 (first entry)  
DT  
XX  
DE Mouse heavy chain variable region scFv seqid 65.  
XX  
KM antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KM heavy chain variable region; single chain antibody; scFv.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-0014486.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
XX (RBGC ) UNIV CALIFORNIA.  
PA  
XX  
XX Marks JD, Amerdorfer P;  
PI  
XX  
XX WPI; 2004-652009/63.  
DR  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
PS Example 1; SEQ ID NO 65; 110pp; English.  
XX  
Cc The invention describes an isolated antibody (I) that specifically binds  
Cc to an epitope specifically bound by an antibody expressed by a specific  
Cc clone where (I) binds to and neutralises botulinum neurotoxin type A  
Cc (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
Cc specifically bound by an antibody expressed by a clone chosen from clone  
Cc S25, C25, C39, 1c6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
Cc 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
Cc neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
Cc comprising BoNT/A neutralising epitope having an epitope that is  
Cc specifically bound by an antibody expressed by clones as mentioned in (I)  
Cc ; producing (I); and a composition (III) comprising several anti-  
Cc botulinum neurotoxin antibodies, where each antibody is specific for a  
Cc different epitope of a botulinum neurotoxin and the combination of  
Cc antibodies shows greater toxin neutralisation than the single antibodies  
Cc in surplus. The following are disclosed: a pharmaceutical composition  
Cc comprising (I); and a kit comprising (I). (I) is useful for neutralising  
Cc BoNT/A antibody and for neutralising a botulinum neurotoxin which

Cc involves contacting neurotoxin with (I) in surplus, where each of (I) is  
Cc specific for a different epitope of the botulinum neurotoxin and the  
Cc combination of antibodies shows greater toxin neutralisation than the  
Cc single antibodies in surplus. (I) is useful for diagnosing the botulism  
Cc or for treating pathologies associated with botulinum neurotoxin  
Cc poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
Cc enables rapid detection or diagnosis of botulism. This is the amino acid  
Cc sequence of a mouse heavy chain variable fragment anti-botulinum toxin  
Cc scFv.  
XX  
SQ Sequence 122 AA;  
XX  
Alignment Scores:  
Pred. No.: 1,45e-53 Length: 122  
Score: 598.50 Matches: 115  
Percent Similarity: 92.13% Conservative: 2  
Best Local Similarity: 90.55% Mismatch: 5  
Query Match: 85.99% Indels: 5  
DB: Gaps: 2  
US-09-403-107-143\_COPY\_1\_381 (1-381) x ADR38663 (1-122)  
Qy 1 GAGGTGCAGCTGCTGAGTGGGAGGCTGGTCCAGCTGGAGGTCCTGAGACTC 60  
Db 1 GluValGlnLeuGlnGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeu 20  
Qy 61 TCTGTGCAAGCTCTGATTCACCTTCAGTAGTATGAGCATGCACTGGCTCCGAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetHisTrrpValArgGlnAla 40  
Qy 121 CCAGCAAGGCGGCTGAGTGGCTGGCTGATTAATCATATGATGAAAGTAATATCAT 180  
Db 41 ProGlyLySGlyLeuGluTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60  
Qy 181 GCAGACTCCGTGAAAGGCGGATTCACCATCTCCAGAGCAATTCAGAACACGCTGAT 240  
Db 61 AlaAspSerValLySGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80  
Qy 241 CTGCAAAATGAAGAGCTGAGCTGAGACACGCGCTGTGTATTAATCTGCGAAATATG 300  
Db 81 LeuGlnMetAsnSerLeuArgIleValAspThrAlaValTyrCysAlaArgAsp--- 99  
Qy 301 GGGTGGGCGAGTGGCTGAGACCTTACTACTACGATATGAGCTGGGCGCAAGG 360  
Db 100 ---TrrpSerGlnGly-----TyrTyrTyrTyrGlyMetAspValTrrpGlyGlnGly 115  
Qy 361 ACCACGGTCACCGCTCTCTCA 381  
Db 116 ThrThrValThrValSerSer 122  
RESULT 7  
ADP22128  
ID ADP22128 standard, protein, 122 AA.  
XX  
XX ADP22128;  
AC  
XX  
XX 09-SEP-2004 (first entry)  
DT  
XX  
DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:34.  
XX  
Cc human; monoclonal antibody; tumour necrosis factor- $\alpha$ ; TNFa;  
Cc anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
Cc antibacterial; antiinflammatory; antipsoriatic; antineumatic;  
Cc eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
Cc neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
Cc TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
Cc bladder cancer; lung cancer; glioblastoma; stomach cancer;  
Cc endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
Cc prostate cancer; immuno-mediated inflammatory disease;  
Cc rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
Cc reestenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
Cc septic shock; cachexia; anorexia; multiple sclerosis.  
XX

OS Homo sapiens.  
 XX  
 PN WO2004050683-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Babcock JS, Kang JS, Foord O, Green L, Peng X, Klakamp S;  
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX  
 DR WPI; 2004-480601/45.  
 DR N-PDB; ADP22127.  
 XX  
 PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 34; 213pp; English.

CC The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNF $\alpha$ ) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNF $\alpha$  in a patient sample, comprising contacting with  
 CC (I), and detecting the level of binding between the antibody and TNF $\alpha$  in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNF $\alpha$  induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antirheumatic,  
 CC antibacterial, antiinflammatory, antipsoaritic, antithrombotic,  
 CC disorder, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNF $\alpha$  antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$   
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 122 AA:

Alignment Scores:  
 Pred. No.: 1.84e-53 Length: 122  
 Score: 597.50 Matches: 114  
 Percent Similarity: 92.91% Conservative: 4  
 Best Local Similarity: 89.76% Mismatches: 5  
 Query Match: 85.85% Indels: 4  
 DB: 8 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x ADP22128 (1-122)

QY 1 GAGGTGAGCTGCTCGAGCTCGGGGAGGCGCTGCTCCAGCTGGAGGCTCCGTGAGACTC 60  
 DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

QY 61 TCGTGTGAGACCTCTGATTCACCTTACAGTACGTATGCGATCGAGTCCGAGGCT 120  
 DB 21 SerCyAlaAlaSerClyPheThrPheSerSerTyRGlyMetHisTrpValArgGlnAla 40  
 QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCGAGTTATATCATATGATGAGAATTAATTAATCTAT 180  
 DB 41 ProGlyLyGlyLeuGlnLutrpValAlaValIleSerTyAspGlySerAsnLyTyTyR 60  
 QY 181 GCAGACTCCGTAAAGGGCCGATTCACCATCTCCAGAGCAATTCACAAGAACGCGTGT 240  
 DB 61 AlaAspSerValIleSerLysPheThrIleSerArgAspAsnSerLysAsnThrLeuTyR 80  
 QY 241 CTGCAATGATGACGCTGAGAGCTGAGAGACGCGCTGTGTATTACTGTGCGAAGATATG 300  
 DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTy-Ty-CyAlaIleArgAspGln 100  
 QY 301 GGGTGGGCGACGTGGAGACCTTACTACTACGCTATGAGAGCTGTGGGCGCAAGGG 360  
 DB 101 -----AspAsnTrpAsn-----TyRTyTyRGlyMetAspValTrpGlyGlnGly 115  
 QY 361 ACCAGGCTGACGCTGCTCTCA 381  
 DB 116 ThrThrValThrValSerSer 122

RESULT 8  
 ADR38664  
 ID ADR38664 standard; peptide; 122 AA.  
 XX  
 AC ADR38664;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Mouse heavy chain variable region scFv seqid 66.

XX anti-bacterial; antibody; botulinum neurotoxin type A; BONT/A.  
 XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 XX heavy chain variable region; single chain antibody; scFv.

XX Mus sp.  
 OS  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 01-AUG-2003; 2003US-00632706.  
 XX  
 PR 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX

PA (REGC ) UNIV CALIFORNIA.

PI Marks JD, Amersdorfer P;  
 XX  
 DR WPI; 2004-652009/63.  
 XX

PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 66; 110pp; English.

PS The invention describes an isolated antibody (I) that specifically binds  
 XX to an epitope specifically bound by an antibody expressed by a specific  
 XX clone where (I) binds to and neutralizes botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-

CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulinum. This is the amino acid  
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin  
 CC scFv.

XX SQ Sequence 122 AA;

Alignment Scores:

Pred. No.:	1,84e-53	Length:	122
Score:	597.50	Matches:	113
Percent Similarity:	92.91%	Conservative:	5
Best Local Similarity:	88.98%	Mismatches:	4
Query Match:	85.85%	Indels:	5
		Gaps:	2

US-09-403-107-143\_COPY\_1\_381 (1-381) x ADR38664 (1-122)

QY 1 GAGTCGACGCTGCTGAGTCTGGGGAGGCGCTGTCAGCCTGGAGGTCCTGAGACTC 60  
 Db 1 GlnIeglnleuLeuGlnSerGlyGlyValValGlnProGlyArgSerleuArgleu 20  
 QY 61 TCTCTGACGCTCTGATTCACCTTCAGTAGCTAGTCAGTGGGTCCTGGAGGCT 120  
 Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyraIaMeHlaItrValArgGlnAla 40  
 QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATGTGATGAAAGTAAATACAT 180  
 Db 41 ProGlyLysGlyLeuGlnItrPalaIaValIleSerTyraPegGlySerAsnLysTyrr 60  
 QY 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGAT 240  
 Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrleuTyrr 80  
 QY 241 CTGCAATGAACAGCCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCCAAGATATG 300  
 Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrIraValTyrrTyrrCysAlaArgAsp--- 99  
 QY 301 GGGTGGGGCAGTGGCTGAGACCCCTACACTACTCGGTATGAGACTGTGGGCCAAGG 360  
 Db 100 ---TTPserGluGly-----TyrrTyrrTyrrGlyMetAspValItrPegGlnGly 115  
 QY 361 ACCAGGTACCGCTCTCTCA 381  
 Db 116 ThrThrValIleValSerSer 122

RESULT 9  
 ADP22222 standard; protein; 126 AA.  
 XX AC ADP22222;  
 XX DT 09-SEP-2004 (first entry)  
 XX XX Human anti-TNFA antibody light chain variable region SEQ ID NO:128.  
 KW human; monoclonal antibody; tumour necrosis factor- $\alpha$ ; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antiproliferative; antineoplastic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
 KW neuroprotective; vasodilator; antileptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;

KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.

OS Homo sapiens.

FN WO2004050683-A2.

PD 17-JUN-2004.

PP 02-DEC-2003; 2003WO-US038281.

PR 02-DEC-2002; 2002US-0430729P.

PA (ABGE-) AGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendschio M, Kathanaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

DR WPI; 2004-480601/45.

DR N-PSDB; ADP22221.

PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor- $\alpha$ , useful for treating neoplastic disease such  
 PT as cancer, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.

PS Example 10; SEQ ID NO 128; 213pp, English.

XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor- $\alpha$  (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (I), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antiproliferative, antineoplastic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotoxic,  
 CC neuroprotective, vasodilator and antileptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 126 AA;

Alignment Scores:

Pred. No.:	3e-53	Length:	126
Score:	595.50	Matches:	113
Percent Similarity:	93.70%	Conservative:	6
Best Local Similarity:	88.98%	Mismatches:	7
Query Match:	85.56%	Indels:	1
		Gaps:	1

US-09-403-107-143\_copy\_1\_381 (1-381) x ADP22222 (1-126)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCTCGAGCTGGAGGTCCTGAGACTC 60  
DB 1 GlnValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGAGCATGAGTGGGTCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTrpGlyMetHisTrpValAlaGlnAla 40  
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCAATTATATCATATGATGAAATAATAATATAT 180  
DB 41 ProGlyLysGlyLeuGlnTrpValAlaValAlaValIleTrpTyrAspGlySerAsnLysTrpTyr 60  
QY 181 GCGAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240  
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80  
QY 241 CTGCAATGAAAGCGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAAGATATG 300  
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValIleTyrCysAlaArgGln--- 99  
QY 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACGTAATGACGTCTGGGCGCAAGG 360  
DB 100 GlyTlAlaValAlaGlyProProTyrTyrTyrTyrGlyMetAspValTrpGlyGlnGly 119  
QY 361 ACCAGCGTCAACCGTCTCTCA 381  
DB 120 ThrThrValThrValSerSer 126

RESULT 10  
AAV82629 standard; protein; 143 AA.

AC AAV82629;  
DT 02-AUG-2000 (first entry)  
XX

Human PTHrP monoclonal antibody clone 5B12-16-12 protein SEQ ID NO:42.  
DE Human PTHrP monoclonal antibody clone 5B12-16-12 protein SEQ ID NO:42.  
XX  
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;  
KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
KW antiarthritic; cytostatic; antiinflammatory.  
XX  
XX Homo sapiens.  
OS  
XX JP2000080100-A.  
PN 21-MAR-2000.  
XX  
XX 12-OCT-1998; 98JP-00304793.  
PF  
XX 17-JUN-1998; 98JP-00188196.  
PR 26-JUN-1998; 98JP-00196729.  
XX  
XX (NIBS ) JAPAN TOBACCO INC.  
PA  
XX WPI; 2000-286723/25.  
DR N-PDB; AAA13939.  
XX  
XX A human monoclonal antibody to parathyroid hormone related protein. -  
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
PT including metastasis, and pain.  
XX  
XX Claim 32; Page 76-77; 88pp; Japanese.  
XX  
XX The present invention describes a human monoclonal antibody to  
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
CC its fragments, following the stimulation of PTHrP has the following  
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
CC the release of calcium from bone; or (c) inhibits elevation of blood

CC calcium content. The monoclonal antibody can be used in the treatment of  
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome  
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
CC antiinflammatory activities. The present sequence represents a human  
CC PTHrP monoclonal antibody clone protein sequence from the present  
CC invention  
XX  
SQ Sequence 143 AA;  
Alignment Scores:  
Pred. No.: 3,91e-53 Length: 143  
Score: 594.50 Matches: 113  
Percent Similarity: 92.13% Conservative: 4  
Best Local Similarity: 88.98 Mismatches: 7  
Query Match: 85.42% Indels: 3  
DB: Gaps: 1

US-09-403-107-143\_copy\_1\_381 (1-381) x AAV82629 (1-143)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCTCGAGCTGGAGGTCCTGAGACTC 60  
DB 20 GlnValGlnLeuValGlnSerGlyGlyGlyValGlnProGlyArgSerLeuArgLeu 39  
QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGAGCATGAGTGGGTCGCCAGGCT 120  
DB 40 SerCysAlaAlaSerGlyPheThrPheSerAsnTrpGlyMetHisTrpValAlaGlnAla 59  
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCAATTATATCATATGATGAAATAATAATATAT 180  
DB 60 ProGlyLysGlyLeuGlnTrpValAlaValAlaValIleTrpTyrAspGlySerAsnLysTrpTyr 79  
QY 181 GCGAGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240  
DB 80 ValAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 99  
QY 241 CTGCAATGAAAGCGCTGAGAGCTGAGACACGCGCTGTATTACTGTGCGAAAGATATG 300  
DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValIleTyrCysAlaArgGln--- 118  
QY 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACGTAATGACGTCTGGGCGCAAGG 360  
DB 119 -----SerSerGlyTrpTyrGlnAspTyrTyrTyrGlyMetAspValTrpGlyGlnGly 136  
QY 361 ACCAGCGTCAACCGTCTCTCA 381  
DB 137 ThrThrValThrValSerSer 143

RESULT 11  
AAV93734 standard; protein; 451 AA.

ID AAV93734  
AC AAV93734;  
DT 03-OCT-2000 (first entry)  
XX  
XX The heavy chain of immunoglobulin clone 11.2.1.  
DE  
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
KW proliferative disorder; cancer; immunodeficient disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO200037504-A2.  
PN 29-JUN-2000.  
XX  
XX 23-DEC-1999; 99WO-US030895.  
PF 23-DEC-1998; 98US-0113647P.  
PR  
XX

PA (PFI2 ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
XX  
XX Hanson DC, Neveu MJ, Mueller EB, Hanke JH, Gilman SC, Davis CG,  
PI Corvalan JR;  
XX  
XX WPI; 2000-442647/38.  
DR N-PSDB; AAA46898.  
XX  
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)  
PT -4 containing specified heavy and light chain sequences, useful for  
XX treating, e.g. immune disorders.  
XX  
XX Claim 2; Fig 22g; 157pp; English.  
XX  
XX The present sequence represents a heavy chain of an antibody of the  
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)  
CC -4. Antibodies of the invention are composed of a heavy chain variable  
CC region, comprising a modified contiguous sequence from a PBI-FR3 sequence  
CC encoded by a human VH3-33 family gene. The modifications are contained in  
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to  
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity  
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and  
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be  
CC used to up-regulate immune system to up-regulate immunodeficient  
CC disorders  
XX  
XX SQ Sequence 451 AA;  
XX  
XX  
XX Alignment Scores:  
XX Pred. No.: 1,15e-52 Length: 451  
XX Score: 591.00 Matches: 113  
XX Percent Similarity: 93.70% Conservative: 6  
XX Best Local Similarity: 88.98% Mismatches: 2  
XX Query Match: 84.91% Indels: 2  
XX DB: 3 Gaps: 1  
XX  
XX US-09-403-107-143\_COPY\_1\_381 (1-381) x AA93734 (1-451)  
XX  
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCCAGCCTGGAGGTCCCTGAGACTC 60  
DB :::: :  
DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCGTGACGCTCTGAGATTCACCTTCAGTACTGAGTACGATGCGGCTCCGAGGCT 120  
DB :  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrglyMetHisTrpValArgGlnAla 40  
QY 121 CCAAGCAAGGGGCTGAGTGGGTGAGCTTATATCATATGATGAAATATAATACATAT 180  
DB :  
DB 41 ProGlyIysGlyLeuGlnTrpValAlaValIleTrpTyraMetGlySerAsnIysTrp 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGACAAATCCAGAGACGCTGTAT 240  
DB :  
DB 61 AlaSerSerValIysGlyArgPheThrIleSerArgAspAsnSerIysAsnThrLeuTy 80  
QY 241 CTGCAAAAGAACGCTGAGAGCTGAGACACGCGTGTGTATTAATCTGCGAAGATATG 300  
DB :  
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValIleTyrcysAlaArgAspPro 100  
QY 301 GGGTGGGCGAGTGGTGGAGACCTTACTACTAGGATGAGAGCTGGGGCCAGAGG 360  
DB :  
DB 101 ArgGlyAlaThrLeuTy-----TyrrTyrrTyrrGlyMetAspValTrpGlyGlnIly 118  
QY 361 ACCAGGTCACCGTCTCTCA 381  
DB :  
DB 119 ThrThrValThrValSerSer 125  
XX  
XX RESULT 12  
XX AAE35889  
XX ID AAE35889 standard; protein; 451 AA.  
XX AC AAE35889;  
XX

DT 17-UN-2003 (first entry)  
XX  
XX Human 11.2.1 anti-CTLA-4 antibody mature heavy chain.  
DE  
XX  
XX Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;  
KM cancer.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 26..35  
FT Region /note="Complementarity determining region (CDR) 1"  
FT Region 50..64  
FT /note="Complementarity determining region (CDR) 2"  
FT Region 100..104  
FT /note="Complementarity determining region (CDR) 3"  
XX  
XX EP1262193-A1.  
XX  
XX 04-DEC-2002.  
XX  
XX 23-MAY-2002; 2002BP-00253652.  
XX  
XX 23-MAY-2001; 2001US-0293042P.  
XX  
XX (PFI2 ) PFIZER PROD INC.  
XX  
XX Hanson DC, Mueller EB;  
XX  
XX WPI; 2003-131215/13.  
XX  
XX N-PSDB; AAD54349.  
XX  
XX Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the  
PT preparation of medicament for the treatment of cancer.  
XX  
XX Disclosure; Fig 1Q; 76pp; English.  
XX  
XX  
XX The invention relates to the use of human anti-cytotoxic T lymphocyte  
CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for  
CC the treatment of cancer such as bone cancer, pancreatic cancer, skin  
CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian  
CC cancer, cancer of the anal region, stomach cancer, breast cancer,  
CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.  
CC The present sequence is human anti-CTLA-4 antibody mature heavy chain  
XX  
XX SQ Sequence 451 AA;  
XX  
XX  
XX Alignment Scores:  
XX Pred. No.: 1,15e-52 Length: 451  
XX Score: 591.00 Matches: 113  
XX Percent Similarity: 93.70% Conservative: 6  
XX Best Local Similarity: 88.98% Mismatches: 2  
XX Query Match: 84.91% Indels: 2  
XX DB: 6 Gaps: 1  
XX  
XX US-09-403-107-143\_COPY\_1\_381 (1-381) x AAE35889 (1-451)  
XX  
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCCAGCCTGGAGGTCCCTGAGACTC 60  
DB :  
DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCGTGACGCTCTGAGATTCACCTTCAGTACTGAGTACGATGCGGCTCCGAGGCT 120  
DB :  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrglyMetHisTrpValArgGlnAla 40  
QY 121 CCAAGCAAGGGGCTGAGTGGGTGAGCTTATATCATATGATGAAATATAATACATAT 180  
DB :  
DB 41 ProGlyIysGlyLeuGlnTrpValAlaValIleTrpTyraMetGlySerAsnIysTrp 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGACAAATCCAGAGACGCTGTAT 240  
DB :  
DB 61 AlaSerSerValIysGlyArgPheThrIleSerArgAspAsnSerIysAsnThrLeuTy 80  
XX

QY 241 CTGCAATGAAACCGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAGATATG 300  
Db 81 LeuGIuMeIaSerneuAlaGluAspThrAlaValTyrTyrCysAlaAspPro 100  
QY 301 GGGTGGGGCAGTGTGAGAGACCTTACTACTACGCTATGACGCTGTGGGCCAAGGG 360  
Db 101 ArgGIyAlaThrLeuTyr-----TyrTyrTyrTyrCylMetAspValTrpGlyGlnGly 118  
QY 361 ACCGAGGTCAACCGTCTCTCTCA 381  
Db 119 ThrThrValThrValSerSer 125  
RESULT 13  
ADS84396  
ID ADS84396 standard; protein; 123 AA.  
XX ADS84396;  
XX  
XX 18-NOV-2004 (first entry)  
XX  
XX Human anti-EPO-R antibody heavy chain variable region SEQ ID NO:35.  
DE human; erythropoietin receptor; EPO receptor;  
XX erythropoietin receptor binding antibody; EPO receptor binding antibody;  
XX antihaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;  
KM wound healing; neural cell damage protection;  
KM neural tissue damage protection; brain injury; spinal cord injury;  
KM stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
XX Homo sapiens.  
XX  
XX W02004035603-A2.  
PN  
XX 29-APR-2004.  
PD  
XX 14-OCT-2003; 2003MO-US032243.  
PF  
XX 14-OCT-2002; 2002US-00269711.  
PR 10-OCT-2003; 2003US-00684109.  
XX  
XX (ABBO ) ABBOTT LAB.  
PA  
PI Deviles PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
XX  
XX WPI: 2004-1348433/32.  
DR N-PSDB; ADS84396.  
XX  
XX New antibodies that bind to or activate an endogenous human  
PT erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
PT anemia.  
XX  
XX Claim 9, SEQ ID NO 35; 192pp; English.  
XX  
XX The present invention describes an antibody or its fragment that binds to  
CC or activates an endogenous activity of a human erythropoietin (EPO)  
XX receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence; and (5) an isolated and  
CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antihaemic, neuroprotective and vulnerary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from

CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence represents a human anti-EPO-R antibody heavy  
CC chain variable region, which is given in the exemplification of the  
CC present invention.  
XX  
XX SQ Sequence 123 AA;  
Alignment Scores:  
Pred. No.: 1,12e-52 Length: 123  
Score: 590.00 Matches: 114  
Percent Similarity: 92.13% Conservative: 3  
Best Local Similarity: 89.76% Mismatches: 6  
Query Match: 84.77% Indels: 4  
DB: Gaps: 1  
US-09-403-107-143\_COPY\_1\_381 (1-381) x ADS84396 (1-123)  
QY 1 GAGGTGACAGTGTGAGTGTGGGGAGGCTGGTCCAGCTGGGAGGTCCTGAGACTC 60  
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuAspLeu 20  
QY 61 TCCTGTGACAGCTGTGATTCACCTTCAGTACTATGCGATGCACTGGCCGACGCT 120  
Db 21 SerCylAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40  
QY 121 CCAAGCAAGGGGCTGAGTGGGTGGCGATTATATCATATGATGAGAACTAATAATCTTT 180  
Db 41 ProGlyLysGlyLeuGlyLeuGlyLeuTrpValAlaValAlaIleSerTyrAspGlySerAsnYsrTyr 60  
QY 181 GCAGACTCCGTGAGAGGGCGGATTCACCATCTCCAGAGACAATTCGAAAGACGCTGT 240  
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80  
QY 241 CTGCAATGAAACCGCTGAGAGCTGAGAGACACGCTGTGTATTACTGTGCGAAGATATG 300  
Db 81 LeuGIuMeIaSerneuAlaGluAspThrAlaValTyrTyrCysAlaLysAsp--- 99  
QY 301 GGGTGGGGCAGTGTGCTGAGAGACCTTACTACTACGCTATGAGCTGTGGGCCAAGGG 360  
Db 100 -----HisGlyGlyArgTyrValTyrAspTyrGlyMetAspValTrpGlyGlnGly 116  
QY 361 ACCGAGGTCAACCGCTCTCTCTCA 381  
Db 117 ThrThrValThrValSerSer 123  
RESULT 14  
ID ADS8538  
ADR68538 standard; protein; 123 AA.  
XX  
XX ADR68538;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Anti-EPO-R-antibody heavy chain variable region seqid 35.  
DE  
XX antihaemic; respiratory; vulnerary; gene therapy; vaccine;  
XX erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
KW wound healing; neural cell damage; tissue damage; brain injury;  
KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;  
KW variable region.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2004175379-A1.  
PN  
XX 09-SEP-2004.  
PD  
XX 10-OCT-2003; 2003US-00684109.  
XX





XX The present sequence is that of a human DP-46 heavy chain variable region  
CC encoded by a human germline DP-46 gene in a transgenic mouse used in  
CC human monoclonal antibody (mAb) construction. A Genviv fusion was  
CC performed using spleen cells from a hybrid mouse containing human  
CC variable and constant region antibody transgenes that was immunised with  
CC recombinant human tumor necrosis factor (TNF) alpha. Human mAbs were  
CC obtained that bound immobilised human TNF alpha with apparently high  
CC avidity. These mAbs had a totally human IgG1, kappa isotype. Their heavy  
CC chain variable region deduced amino acid sequences (see AAM51168-72)  
CC showed high similarity to the DP-46 sequence. The invention provides  
CC isolated human, primate, rodent, mammalian, chimeric, humanised and/or  
CC complementarity determining region (CDR)-grafted anti-TNF antibodies,  
CC immunoglobulins, and cleavage products and variants, as well as anti-TNF  
CC antibody compositions, encoding or complementary nucleic acids, vectors,  
CC host cells, compositions, formulations, devices, transgenic animals,  
CC transgenic plants, and methods of making and using them. The anti-TNF  
CC antibody comprises at least a portion of an immunoglobulin molecule,  
CC especially the heavy chain and/or light chain variable regions given in  
CC the present sequence and in AAM5165, or either all of the CDRs of the  
CC heavy chain (see AAM5158-60) or all of the CDRs of the light chain (see  
CC AAM5161-63). The antibodies may inhibit TNF-induced cell adhesion  
CC molecules, inhibit TNF binding to receptor, or provide Arthritic Index  
CC improvement in a mouse model. They are useful for diagnosing or treating  
CC a TNF related condition in a cell, tissue, organ or animal (claimed) such  
CC as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,  
CC Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular  
CC disease such as arteriosclerosis, atherosclerosis, restenosis, angina  
CC pectoris or myocardial infarction, an infectious disease in a cell such  
CC as bacterial, viral, and fungal infections, pneumonia, leprosy and  
CC malaria, a malignant lymphoma such as leukaemia, chronic myelocytic  
CC leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological  
CC disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,  
CC Alzheimer's disease and Creutzfeldt-Jakob disease

XX Sequence 118 AA:

## Alignment Scores:

Pred. No.:	1,25e-52	Length:	118
Score:	589.50	Matches:	113
Percent Similarity:	91.34%	Conservative:	3
Best Local Similarity:	88.98%	Mismatches:	2
Query Match:	84.70%	Indels:	9
DB:	5	Gaps:	1

US-09-403-107-143\_COPY\_1\_381 (1-381) x AAM51167 (1-118)

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QY 61 TCCTGTCGACGCTCTGATTCACCTTCAGTATGAGCATGAGTCGCGCCGAGGCT 120  
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Db 21 SerCys[Ala]IaSer[Gl]yPheTrpPheSer[Ser]TrpAlaMet[His]TrpVal[Arg]GlnAla 40  
QY 121 CCAGGCAGAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAATATAATACTAT 180  
|||||  
Db 41 Pro[Gl]yPhe[Gl]yLeu[Gl]uTrpVal[Ala]Val[Ala]Ser[Trp]Asp[Gl]ySer[Asn]y[Ser]TrpTyr 60  
QY 181 GCAGACTCCGTCGAGAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGAT 240  
|||||  
Db 61 AlaAsp[Ser]Val[Ala]ySer[Gl]yArgPheTrp[His]LeuSer[Arg]Asp[Asn]Ser[Leu]y[Asn]ThrLeuTyr 80  
QY 241 CTGCAATGTAACAGCTGAGAGAGTCGAGAGACAGCGTGATTAATGCGAAAGATATG 300  
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Db 81 Leu[Gl]nMet[Asn]Ser[Leu]ArgAla[Gl]uAsp[Thr]AlaVal[Trp]Tyr[Cys]Ala----- 97  
QY 301 GGGTGGGGCAGTGGCTGAGACCTTACTACTACTACGATGACGTCGTGGGCGCAAGGG 360  
|||  
Db 98 -----ArgTrpTyrTrpTyrTrp[Gl]yMet[Asp]Val[Trp]Gl[y]GlnGly 111  
QY 361 ACCACGGTCACCGTCTCTCA 381  
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Db 112 ThrThrValThrValSerSer 118

Search completed: August 29, 2005, 11:37:18  
Job time : 98.5214 secs



GenCore version 5.1.6  
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## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 20.3526 Seconds

(without alignments)  
2794.861 Million cell updates/sec

Title: US-09-403-107-143\_COPY\_1\_381

Perfect score: 696  
Sequence: 1 gaggtgcagctgcgcagtc.....ccacgctcacctctctctca 381

## Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool\_p/US09403107/runat\_29082005\_120125\_18914/app\_query.fasta\_1.1038  
-DB=Issued Patents AA -QEMT=faetan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591	84.9	451	US-09-472-087-70	Sequence 70, App1
2	581.5	83.5	126	US-09-240-274-26	Sequence 26, App1
3	575.5	82.7	126	US-09-240-274-153	Sequence 153, App1
4	573.5	82.4	126	US-09-240-274-25	Sequence 25, App1
5	570	81.9	123	US-09-424-840B-6	Sequence 6, App1
6	558.5	80.2	124	US-09-424-840B-16	Sequence 16, App1
7	554	79.6	167	US-09-472-087-80	Sequence 80, App1
8	553.5	79.5	310	US-09-079-029-11	Sequence 11, App1
9	552.5	79.4	128	US-09-840-459-77	Sequence 77, App1
10	552.5	79.4	128	US-09-840-459-79	Sequence 79, App1
11	552.5	79.4	128	US-09-497-625A-77	Sequence 77, App1
12	552.5	79.4	128	US-09-497-625A-79	Sequence 79, App1

13	552	79.3	125	3	US-09-240-274-140	Sequence 140, App
14	547	78.6	120	1	US-07-942-245-35	Sequence 35, App1
15	546	78.4	123	4	US-09-560-198A-2	Sequence 2, App1
16	545	78.3	119	1	US-08-331-398A-46	Sequence 46, App1
17	545	78.3	119	2	US-08-331-397B-46	Sequence 46, App1
18	545	78.3	119	2	US-08-759-804A-46	Sequence 46, App1
19	545	78.3	119	3	US-09-227-693-46	Sequence 46, App1
20	544.5	78.2	126	3	US-09-240-274-152	Sequence 152, App
21	543	78.0	115	4	US-09-726-219A-167	Sequence 167, App
22	542	77.9	117	3	US-09-025-769B-24	Sequence 24, App1
23	542	77.9	117	4	US-09-490-070A-24	Sequence 24, App1
24	542	77.9	117	4	US-09-490-153-24	Sequence 24, App1
25	542	77.9	117	4	US-09-490-324-24	Sequence 24, App1
26	542	77.9	125	4	US-09-840-459-84	Sequence 84, App1
27	542	77.8	125	4	US-09-497-625A-84	Sequence 84, App1
28	541.5	77.8	126	3	US-09-240-274-13	Sequence 13, App1
29	541.5	77.8	126	3	US-09-240-274-16	Sequence 16, App1
30	541.5	77.8	126	3	US-09-240-274-147	Sequence 147, App
31	541.5	77.8	126	3	US-09-240-274-148	Sequence 148, App
32	540.5	77.7	126	3	US-09-240-274-146	Sequence 146, App
33	540	77.6	125	3	US-09-240-274-8	Sequence 8, App1
34	540	77.6	125	3	US-09-240-274-20	Sequence 20, App1
35	540	77.6	125	3	US-09-240-274-21	Sequence 21, App1
36	540	77.6	125	3	US-09-240-274-22	Sequence 22, App1
37	540	77.6	167	4	US-09-472-087-9	Sequence 9, App1
38	539	77.4	125	4	US-09-840-459-76	Sequence 76, App1
39	539	77.4	125	4	US-09-497-625A-76	Sequence 76, App1
40	538.5	77.4	123	3	US-08-983-607-38	Sequence 38, App1
41	537.5	77.2	174	4	US-09-472-087-12	Sequence 12, App1
42	536.5	77.1	126	3	US-09-240-274-14	Sequence 14, App1
43	536.5	77.1	126	3	US-09-240-274-15	Sequence 15, App1
44	536	77.0	225	4	US-09-456-090A-108	Sequence 108, App
45	536	77.0	225	4	US-09-453-234-108	Sequence 108, App

## ALIGNMENTS

RESULT 1  
US-09-472-087-70  
; Sequence 70, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEYEU, MARK J.  
; APPLICANT: MEYER, EILEEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-70  
Alignment Scores:  
Pred. No.: 5.99e-59  
Score: 591.00  
Percent Similarity: 93.70%  
Best Local Similarity: 88.98%  
Query Match: 84.91%  
DB: 4  
Length: 451  
Matches: 113  
Conservative: 6  
Mismatch: 2  
Indels: 1  
Gaps: 1  
US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-472-087-70 (1-451)

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Db      1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuAlaGlu 20
QY      61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCGGTCGCCAGGCT 120
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      21 SerCyAlaAlaSerGlyPheThrPheSerSerGlyMetHisTrpValArgGlnAla 40
QY      121 CCAAGCAAGGGGCTGAGTGGGGGCGAGTATATCATATGATGAGTAAATATCTAT 180
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      41 ProGlyLysGlyLeuGlnTrpValAlaValAlaLeuTrpTyrAspGlySerAsnLysHisTrp 60
QY      181 GCAGACTCCGCTGAAGGGCCGATTCCACCATCTCCAGAGACAATCCAGAACGCTGTAT 240
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      61 AlaAspSerValLysGlyArgPheThrLileSerArgAspAsnSerLysAsnThrLeuTyr 80
QY      241 CTCGAATGAACAGCTGTGAGAGCTGAGAGACAGCGCTGTGTATTACTGTGCGAAAGATATG 300
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      81 LeuGlnMetAspSerLeuArgAlaGlnAspThrAlaValTyrCysAlaArgAspPro 100
QY      301 GGGTGGGCGAGTGGCTGAGACACCTTACTACTACTAGCTATGACGCTGGGCGCAAGG 360
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      101 ArgGlyAlaThrLeuTyr-----TyrTyrTyrTyrGlyMetAspValTrpGlyGlnGly 118
QY      361 ACCAGCGTCACCGTCTCTCTCA 381
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      119 ThrThrValThrValSerSer 125
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## RESULT 2

```
US-09-240-274-26
; Sequence 26, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26
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## Alignment Scores:

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Pred. No.: 4,73e-58
Score: 581.50
Percent Similarity: 93.70%
Best Local Similarity: 86.61%
Query Match: 83.55%
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DB: 3

Length: 126  
Matches: 110  
Conservative: 9  
Mismatch: 7  
Indels: 1  
Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-240-274-26 (1-126)

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QY      1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCACGCTGGAGAGTCCCTGAGACTC 60
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Db      1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuAlaGlu 20
QY      61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCGGTCGCCAGGCT 120
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      21 SerCyAlaAlaSerGlyPheThrPheSerSerGlyMetHisTrpValArgGlnAla 40
QY      121 CCAAGCAAGGGGCTGAGTGGGGGCGAGTATATCATATGATGAGTAAATATCTAT 180
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
```

```
Db      41 ProGlyLysGlyLeuGlnTrpValAlaValAlaValTyrTyrAspGlySerAsnLysHisTrp 60
QY      181 GCAGACTCCGCTGAAGGGCCGATTCCACCATCTCCAGAGACAATCCAGAACGCTGTAT 240
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      61 SerAspSerValLysGlyArgPheThrLileSerArgAspAsnSerLysAsnThrLeuTyr 80
QY      241 CTCGAATGAACAGCTGTGAGAGCTGAGAGACAGCGCTGTGTATTACTGTGCGAAAGATATG 300
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      81 LeuGlnMetAspSerLeuArgAlaGlnAspThrAlaValTyrCysAlaArgAlaGlnArg 100
QY      301 GGGTGGGCGAGTGGCTGAGACACCTTACTACTACTAGCTATGACGCTGGGCGCAAGG 360
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      101 AsnPheArgSerGlyTyr---SerArgTyrTyrTyrGlyMetAspValTrpGlyProGly 119
QY      361 ACCAGCGTCACCGTCTCTCTCA 381
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      120 ThrThrValThrValSerSer 126
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## RESULT 3

```
US-09-240-274-153
; Sequence 153, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-153
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## Alignment Scores:

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Pred. No.: 2.3e-57
Score: 575.50
Percent Similarity: 92.91%
Best Local Similarity: 85.83%
Query Match: 82.69%
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DB: 3

Length: 126  
Matches: 109  
Conservative: 9  
Mismatch: 8  
Indels: 1  
Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-240-274-153 (1-126)

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QY      1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCACGCTGGAGAGTCCCTGAGACTC 60
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Db      1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuAlaGlu 20
QY      61 TCCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCGGTCGCCAGGCT 120
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      21 SerCyAlaAlaSerGlyPheThrPheSerSerGlyMetHisTrpValArgGlnAla 40
QY      121 CCAAGCAAGGGGCTGAGTGGGGGCGAGTATATCATATGATGAGTAAATATCTAT 180
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      41 ProGlyLysGlyLeuGlnTrpValAlaValAlaValTyrTyrAspGlySerAsnLysHisTrp 60
QY      181 GCAGACTCCGCTGAAGGGCCGATTCCACCATCTCCAGAGACAATCCAGAACGCTGTAT 240
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      61 SerAspSerValLysGlyArgPheThrLilePheArgAspAsnSerLysAsnThrLeuTyr 80
QY      241 CTCGAATGAACAGCTGTGAGAGCTGAGAGACAGCGCTGTGTATTACTGTGCGAAAGATATG 300
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Qy 301 GGGTGGGAGCTGCTGAGAGACCTACTACTAGGATGAGCTGGGGCCAGAGG 360  
Db 101 AenpheargSerGlyTyr---SerargTyrTyrGlyMetAspValTrpGlyProGly 119  
Qy 361 ACCACGGTCACCGTCTCTCA 381  
Db 120 ThrThrValThrValSerSer 126

## RESULT 4

US-09-240-274-25  
; Sequence 25, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain D30  
US-09-240-274-25

## Alignment Scores:

Pred. No.:	3,896-57	Length:	126
Score:	573.50	Matches:	109
Percent Similarity:	92.91%	Conservative:	9
Best Local Similarity:	85.83%	Mismatches:	8
Query Match:	82.40%	Indels:	1
DB:	3	Gaps:	1

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-240-274-25 (1-126)

Qy 1 GAGGTGAGCTGCTGAGATCTGGGGAGCCCTGCTCCAGCTGAGAGCTCCCTGAGATC 60  
Db 1 GlnValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
Qy 61 TCTGTGAGCCTCTGATTCACCTTACGTAGCTATGAGCATGACCTGGTCCGACGAGCT 120  
Db 21 SerGlyAlaAlaSerGlyPheThrPheSerSerTyrGlyMetArgTrpValArgGlnAla 40  
Qy 121 CCAGGCAAGGGGCTGAGTGGCTGAGCTATATCATATGATGAGAGTAATTAATATCAT 180  
Db 41 ProGlyGlyGlyLeuGlnTrpValAlaValAlaValTyrTrpArgGlySerAlaLeuHisTyr 60  
Qy 181 GCAGACTCCGCTGAGAGGGCCGATTCACCATCTCCAGAGACATTCGAAAGACGCTGAT 240  
Db 61 SerArgSerValTyrGlyArgPheThrIleSerArgAspAsnSerValAsnThrLeuTyr 80  
Qy 241 CTGCAATGACACAGCTGAGAGCTGAGACACGCGTGTGATTAATCTGCGAAGATATG 300  
Db 81 LeuGlnMetAspSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgGlnArg 100  
Qy 301 GGGTGGGAGCTGCTGAGAGACCTACTACTAGGATGAGCTGGGGCCAGAGG 360  
Db 101 AenpheargSerGlyTyr---SerargTyrTyrGlyMetAspValTrpGlyProGly 119  
Qy 361 ACCACGGTCACCGTCTCTCA 381  
Db 120 ThrThrValThrValSerSer 126

## RESULT 5

US-09-424-840B-6

; Sequence 6, Application US/09424840B  
; Patent No. 6790938  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424,840B  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1  
; PRIOR FILING DATE: 1998-05-08  
; PRIOR APPLICATION NUMBER: DE 19755227.7  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: DE 19723904.8  
; PRIOR FILING DATE: 1997-06-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-424-840B-6

## Alignment Scores:

Pred. No.:	9,716-57	Length:	123
Score:	570.00	Matches:	111
Percent Similarity:	91.41%	Conservative:	6
Best Local Similarity:	86.72%	Mismatches:	5
Query Match:	81.90%	Indels:	6
DB:	4	Gaps:	3

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-424-840B-6 (1-123)

Qy 1 GAGGTGAGCTGCTGAGATCTGGGGAGCCCTGCTCCAGCTGAGAGCTCCCTGAGATC 60  
Db 1 GlnValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
Qy 61 TCTGTGAGCCTCTGATTCACCTTACGTAGCTATGAGCATGACCTGGTCCGACGAGCT 120  
Db 21 SerGlyAlaAlaSerGlyPheThrPheSerSerTyrGlyMetArgTrpValArgGlnAla 40  
Qy 121 CCAGGCAAGGGGCTGAGTGGCTGAGCTATATCATATGATGAGAGTAATTAATATCAT 180  
Db 41 ProGlyGlyGlyLeuGlnTrpValAlaValAlaValTyrTrpArgGlySerAlaLeuHisTyr 60  
Qy 181 GCAGACTCCGCTGAGAGGGCCGATTCACCATCTCCAGAGACATTCGAAAGACGCTGAT 240  
Db 61 AlaAspSerValTyrGlyArgPheThrIleSerArgAspAsnSerValAsnThrLeuTyr 80  
Qy 241 CTGCAATGACACAGCTGAGAGCTGAGACACGCGTGTGATTAATCTGCGAAGATATG 300  
Db 81 LeuGlnMetAspSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgGlnArg 100  
Qy 301 GGG---TGGGGAGCTGCTGAGAGACCTACTACTAGGATGAGCTGGGGCCAGAGG 360  
Db 101 GlySerTrpGly---GlyTrpAspPheTyr-----MetAspValTrpGlyLys 115  
Qy 358 GGGACACGGTCACCGTCTCTCA 381  
Db 116 GlyThrThrValThrValSerSer 123

## RESULT 6

US-09-424-840B-16  
; Sequence 16, Application US/09424840B  
; Patent No. 6790938  
; GENERAL INFORMATION:  
; APPLICANT: Berchtold, Peter  
; APPLICANT: Escher, Robert F. A.  
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES  
; FILE REFERENCE: 100564-09049  
; CURRENT APPLICATION NUMBER: US/09/424,840B  
; CURRENT FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: DE 19820663.1

PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: DE 19755227.7  
PRIOR FILING DATE: 1997-12-12  
PRIOR APPLICATION NUMBER: DE 19723904.8  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patent version 3.1  
SEQ ID NO 16  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-424-840B-16

Alignment Scores:  
Pred. No.: 2 01e-55  
Score: 558.50  
Percent Similarity: 90.53%  
Best Local Similarity: 86.61%  
Query Match: 80.24%  
Length: 124  
Matches: 110  
Conservative: 5  
Mismatch: 9  
Indels: 3  
Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-424-840B-16 (1-124)

QY 1 GAGGTGACGCTGCTGAGTCTGGGAGGCGCTGCTGACGCTGGAGGCTGCTGAGATTC 60  
Db 1 GlnValIylLeuIeuIuSerIyGlyGlyValIAlHIsProGlyIArgSerLeuIArgLeu 20  
QY 61 TCGTGTGACGCTCTGATTCACCTTCAGTACGTATGAGCATGAGCGGCTCCGCGGCT 120  
Db 21 SerCysAlaIAserGlyPheThrPheSerSerIyThrMetHIsTrpValAlArgGlnAla 40  
QY 121 CCAAGCAAGGGGCTGAGTGGTGGCAGTATATCATATGATGAGATGATAATATACTAT 180  
Db 41 ProGlyIylSerIyLeuGluIuTrpValAlAlaIleuIleSerIyIAspIylSerHenuIyIy 60  
QY 181 GCAGACTCCGCTGAGGCGGCGGATTCACCATCTCCAGAGCAATTCAGAAACAGCTGTAT 240  
Db 61 AlaAspSerValIylSerGlyArgPheAlaIleSerArgAspHenuIySerIySantHrLeuIy 80  
QY 241 CTGCAATATGAACGCTGAGAGGCTGAGAGACGCTGTGATATCTGCGAAGATATG 300  
Db 81 LeuGlnMetHenuIySerLeuAlaGluAspThrAlaValIyIyCysAlaIylAspGly 100  
QY 301 GGGTGGGCGAGTGGTGGAGACCTTACTACTAGCGTATGAGCGTCTGGGCGCAAGG 360  
Db 101 ArgSerGlySerIyIyAlaIyG-----PheAspIylMetHenuIyIyIyGlnGly 117  
QY 361 ACCAGCGTACCGCTTCTCTCA 381  
Db 118 ThrThrValThrValSerSer 124

RESULT 7  
US-09-472-087-80  
Sequence 80, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILEEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PFI  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 80  
LENGTH: 167

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-80

Alignment Scores:  
Pred. No.: 7.29e-55  
Score: 554.00  
Percent Similarity: 93.22%  
Best Local Similarity: 89.83%  
Query Match: 79.60%  
Length: 167  
Matches: 106  
Conservative: 4  
Mismatch: 6  
Indels: 2  
Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-472-087-80 (1-167)

QY 28 GAGCTGTGACGCTGAGGAGGCTCCCTGAGACTCTCTGAGACGCTGAGATTCACCTTC 87  
Db 1 GlnValIAlGlnProGlyIArgSerLeuIuIleuSerCysAlaIleSerGlyPheThrIle 20  
QY 88 AGTACGTATGAGCATGAGTGGTCCGCGAGGCTCCAGGCGAAGGGCTGAGTGGTGCA 147  
Db 21 SerSerIyIyGlyMetHIsTrpValAlArgGlnAlaProGlyIylSerGlyLeuGluIuTrpValAla 40  
QY 148 GTTATATCATATGATGAGATGATAATATCTATGACAGACTCCGCTGAGAGGCGGATTCACC 207  
Db 41 ValIleIyIyIyAspGlySerHenuIyIyIyAlaAspSerValIylSerIyIyArgPheThr 60  
QY 208 ATCTCCAGAGCAATTCAGAAACGCTGTATCTGCAATGAAACAGCTGAGACTGAG 267  
Db 61 IleSerArgAspAspSerIySantHrLeuIyIyLeuGlnMetHenuIySerIyLeuArgAlaGlu 80  
QY 268 GACAGCGCTGTATCTGCTGCGAAGATATGAGGCTGGGCGAGTGGCTGAGACCTTAC 327  
Db 81 AspThrAlaValIyIyIyCysAlaIylArgAspProArgGlyAlaThrLeuIyIy-----Tyr 98  
QY 328 TACTACTACGATGAGCTCTGGGCGCAAGGAGCAGCGTATCCGCTCTCTCTCA 381  
Db 99 TyrIyIyIyGlyMetAspValIy 116

RESULT 8  
US-09-079-029-11  
Sequence 11, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 11:

```
SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-11

Alignment Scores:
Pred. No.: 1,036-54 Length: 310
Score: 553.50 Matches: 106
Percent Similarity: 88.19% Conservative: 6
Best Local Similarity: 83.46% Mismatches: 6
Query Match: 79.53% Indels: 9
DB: 3 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-079-029-11 (1-310)

QY 1 GAGGTGCAAGCTGCTGAGTCTGGGGAGGCGCTGCTCAGCCTGGAGGTCCTGAGACTC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 40 GlnValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 59
QY 61 TCCTGTGAGCCTCTGAGATTCACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGCT 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 60 SerCysAlaAlaSerGlyPheLeuPheSerSerTyrglyMetHisTrpValArgGlnAla 79
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGCAATTATATCATATGATGAATATAATATACTAT 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 80 ProGlyLysGlyLeuGlnTrpValAlaGlyIlePheTyraSPGlyAlaSerLysTyrr 99
QY 181 GCAGATCCGTGAAAGGCGGATTCACATCTCCAGAGACAATTCACAGAACAGCTGTAT 240
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 100 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrr 119
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGACACAGCGCTGTGATTACTGTGCGAAAGATATG 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 120 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrrCysAlaArgAspArg 139
QY 301 GGGTGGGGCAGTGGCTGGAGACCCACTACTACGAGTAATGGAGAGCTGCGGGCCCAAGG 360
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 140 Gly-----TyrTyrrTyrrMetAspValTrpGlyGln 150

QY 361 ACCAGCGTACCGTCTCTCA 381
DB 151 ThrThrValThrValSerSer 157

RESULT 9
US-09-840-459-77
; Sequence 77, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 128
; TYPE: PRT
```

```
ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1) ... (128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-77

Alignment Scores:
Pred. No.: 9,896-55 Length: 128
Score: 552.50 Matches: 109
Percent Similarity: 86.72% Conservative: 2
Best Local Similarity: 85.16% Mismatches: 16
Query Match: 79.38% Indels: 1
DB: 4 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-09-840-459-77 (1-128)

QY 1 GAGGTGCAAGCTGCTGAGTCTGGGGAGGCGCTGCTCAGCCTGGAGGTCCTGAGACTC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1 GlnValGlnLeuValGlnSerGlyGlyValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGAGCCTCTGAGATTCACTTCAGTAGCTATGGCATGCACTGGTCCGCAAGCT 120
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrglyMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGCAATTATATCATATGATGAATATAATATACTAT 180
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 41 ProGlyLysGlyLeuGlnTrpValSerAlaIleSerGlySerGlySerThrTyrr 60
QY 181 GCAGATCCGTGAAAGGCGGATTCACCATCTCCAGAGACAATTCACAGAACAGCTGTAT 240
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrr 80
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGACACAGCGCTGTGATTACTGTGCGAAAGATATG 300
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrrCysAlaArgAspArg 100
QY 301 GGGTGGGGCAGTGGCTGGAGACCCACTACTACTACGAGTAATGGAGAGCTGCGGGCCCA 357
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 101 ArgAsnTyraSPheTrpSerGly**TyrTyrrTyrrGlyMetAspValTrpGlyGln 120

QY 358 GGGACGACGGTACCGTCTCTCA 381
DB 121 GlyThrThrValThrValSerSer 128

RESULT 10
US-09-840-459-79
; Sequence 79, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-403-107-143_copy_1_381 (1-381) x US-09-840-459-79 (1-128)

Alignment Scores:
Pred. No.: 9,89e-55 Length: 128
Score: 552.50 Matches: 109
Percent Similarity: 86.72% Conservative: 2
Best Local Similarity: 85.16% Mismatches: 16
Query Match: 79.38% Indels: 1
DB: 4 Gaps: 1

US-09-403-107-143_copy_1_381 (1-381) x US-09-840-459-79 (1-128)
QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCGAGCTCGAGAGTCCCTGAGACTC 60
Db 1 GluValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlySerLeuArgLeu 20
QY 61 TCCGTGACGCTCTGTGATTCACTTCAGTAGCTAGTCATGCACTGGGTCGCCAGGCT 120
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnIla 40
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAGTAAATACTAT 180
Db 41 ProGlyLyGlyLeuGlnTrpValSerAlaIleSerGlySerGlySerThrTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACCATCTCGAGAGCAATTCAGAGACGCTGTAT 240
Db 61 AlaAspSerValLyGlyArgPheThrIleSerArgAspAsnSerLyAsnThrLeuTyr 80
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAGATAG 300
Db 81 LeuGlnMetCAsnSerLeuArgAlaGlnAspThrAlaValTyrCysAlaIaIaAspArg 100
QY 301 GGGTGGGGCAGTGGCTGGAGA---CCCTACTACTACAGGTAGGAGCGCTGGGGCCAA 357
Db 101 ArgAsnTyrAspPheTrpSerGly**TyrTyrTyrTyrGlyMetAspValTrpGlyGln 120
QY 358 GGGACCAAGGCTCACCGCTCTCTCA 381
Db 121 GlyThrThrValThrValSerSer 128

RESULT 11
US-09-497-625A-77
; Sequence 77, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Xaa = Any Amino Acid
```

```

; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-497-625A-77

Alignment Scores:
Pred. No.: 9,89e-55 Length: 128
Score: 552.50 Matches: 109
Percent Similarity: 86.72% Conservative: 2
Best Local Similarity: 85.16% Mismatches: 16
Query Match: 79.38% Indels: 1
DB: 4 Gaps: 1

US-09-403-107-143_copy_1_381 (1-381) x US-09-497-625A-77 (1-128)
QY 1 GAGGTGACGCTGCTCGAGTCTGGGGAGGCGCTGCGAGCTCGAGAGTCCCTGAGACTC 60
Db 1 GluValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlyLySerLeuArgLeu 20
QY 61 TCCGTGACGCTCTGTGATTCACTTCAGTAGCTAGTCATGCACTGGGTCGCCAGGCT 120
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnIla 40
QY 121 CCAAGGCAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAGTAAATACTAT 180
Db 41 ProGlyLyGlyLeuGlnTrpValSerAlaIleSerGlySerGlyLySerThrTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACCATCTCGAGAGCAATTCAGAGACGCTGTAT 240
Db 61 AlaAspSerValLyGlyArgPheThrIleSerArgAspAsnSerLyAsnThrLeuTyr 80
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAGATAG 300
Db 81 LeuGlnMetCAsnSerLeuArgAlaGlnAspThrAlaValTyrCysAlaIaIaAspArg 100
QY 301 GGGTGGGGCAGTGGCTGGAGA--CCCTACTACTACTACGATGATGAGACGCTGGGGCCAA 357
Db 101 ArgAsnTyrAspPheTrpSerGly**TyrTyrTyrTyrGlyMetAspValTrpGlyGln 120
QY 358 GGGACCAAGGCTCACCGCTCTCTCA 381
Db 121 GlyThrThrValThrValSerSer 128

RESULT 12
US-09-497-625A-79
; Sequence 79, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
```

US-09-497-625A-79

## Alignment Scores:

Pred. No.: 9,89e-55 Length: 128  
Score: 552.50 Matches: 109  
Percent Similarity: 86.72% Conservative: 2  
Best Local Similarity: 85.16% Mismatches: 16  
Query Match: 79.38% Indels: 1  
DB: 4 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-497-625A-79 (1-128)

QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCTGTGTCAGCTGGAGGTCCTGAGACTC 60  
DB 1 GIVVAGINLEUHGILSERGLYGLYLEUVALGINPROGLYGLYSERLEUARGLEU 20  
QY 61 TCTGTGAGGCTCTGATTCACCTTCAGTACCTATGCGATGACCTGGGTCGCCAGGCT 120  
DB 21 SERCYSAIAAASERGLYPHERPHERSERSEYRYALAMETSEYTRIPVALARGINLA 40  
QY 121 CCAAGCAAGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAACTAT 180  
DB 41 PROGLYVSGLYLEUGLUTRIPVALSERIALISERGLYSEYRGLYSEYRTHRYTYR 60  
QY 181 GCAGACTCGGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCCAGAGACGCTGTAT 240  
DB 61 AIAAPSERVALYVGLYARGPHERTHRIESEYRARGAPASERLYASANTHRIEUYR 80  
QY 241 CTGCAATGAAACAGCTGAGCTGAGAGCAAGCTGTGTATTACTGTGCGAAGATATG 300  
DB 81 LEUGINMETANSEYRLEUARGALAGLUNAPHTHALAVALTYRYCYBALALYASAPRG 100  
QY 301 GGGTGGGAGCTGGCTGAGA---CCCTACTACTACTACGGTATGAGACGCTGGGGCCAA 357  
DB 101 ARGANTYRASPHERTRIPSEYR\*\*TYRYTYRYTYRYGLYMETASPVALTIPGLYGLN 120  
QY 358 GGGACACGAGCTCACCGCTCTCTCA 381  
DB 121 GLYTHRTHTVALTHVALSER 128

## RESULT 13

US-09-240-274-140  
; Sequence 140, Application US/09240274  
; Patent No. 6255455

## GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
EARLIER FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 140  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH16  
US-09-240-274-140

## Alignment Scores:

Pred. No.: 1.12e-54 Length: 125  
Score: 552.00 Matches: 106  
Percent Similarity: 90.55% Conservative: 9  
Best Local Similarity: 83.46% Mismatches: 10  
Query Match: 79.31% Indels: 2  
DB: 3 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-240-274-140 (1-125)

QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCTGTGTCAGCTGGAGGTCCTGAGACTC 60  
DB 1 GIVVAGINLEUHGILSERGLYGLYVALVALGINPROGLYARGSERLEUARGLEU 20  
QY 61 TCTGTGAGGCTCTGATTCACCTTCAGTACCTATGCGATGACCTGGGTCGCCAGGCT 120  
DB 21 SERCYSAIAAASERGLYPHERPHERSERSEYRYGLYMETSEYTRIPVALARGINLA 40  
QY 121 CCAAGCAAGGGCTGAGTGGGTGGCAGTTATATCATATGATGAAAGTAATAACTAT 180  
DB 41 PROGLYARGLYLEUGLUTRIPVALALALEULETRIPYRASPGLYASANTHRYTYR 60  
QY 181 GCAGACTCGGTGAAGGGCGGATTCACCATCTCCAGAGCAATTCCAGAGACGCTGTAT 240  
DB 61 AIAAPSERVALYVGLYARGPHERPHERSERSEYRYALAMETSEYTRIPVALARGINLA 80  
QY 241 CTGCAATGAAACAGCTGAGCTGAGAGCAAGCTGTGTATTACTGTGCGAAGATATG 300  
DB 81 LEUGINMETANSEYRLEUARGALAGLUNAPHTHALAVALTYRYCYBALALYASAPGLN 100  
QY 301 GGGTGGGAGCTGGCTGAGAGCCTACTACTACTACGATGATGAGACGCTGGGGCCAA 360  
DB 101 ARGALALALAGLY-----LIEPHERTYRYSERARGMETASPVALTIPGLYGLN 118  
QY 361 ACACGCTCACCGCTCTCTCA 381  
DB 119 THRTRVALTHVALSER 125

## RESULT 14

US-07-942-245-35  
; Sequence 35, Application US/07942245  
; Patent No. 5639641

## GENERAL INFORMATION:

APPLICANT: PEDERSEN, Jan T.  
APPLICANT: REES, Anthony R.  
APPLICANT: ROGUSKA, Michael A.  
APPLICANT: GUID, Braydon C.  
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
NUMBER OF SEQUENCES: 522  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: HP 9000/700 Workstation  
OPERATING SYSTEM: UNIX  
SOFTWARE: in house  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/942,245  
FILING DATE: 09-SEP-1992  
CLASSIFICATION: 530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 649103  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-942-245-35

## Alignment Scores:

Pred. No.: 4.12e-54 Length: 120

Score: 547.00 Matches: 107  
Percent Similarity: 85.27% Conservative: 3  
Best Local Similarity: 82.95% Mismatches: 7  
Query Match: 78.59% Indels: 12  
DB: 1 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-07-942-245-35 (1-120)

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QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGACGCTGGAGGCTCCCTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGGATTCACTTCAGTAGCTATGACATGACATGCGGATCCGCGAGCT 120
Db 21 SerCyAlaAlaSerGlyPheThrPheSerSerTyrAlaMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGGAGTGGGTGGGCAATTATCATATGATGAAGTAATAATCTAT 180
Db 41 ProGlyLyseGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATCCAGAACAAGCGCTGTAT 240
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGTGTGTATTACTGTGCG----- 291
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgAspArg 100
QY 292 AAGGATATGGGGTGGGGGAGTGGCTGAGACCTACTACTACTACGATATGACGCTCTGG 351
Db 101 LysAspTrpGlyTyrTrpAlaLeu-----PheAspTyrTyr 111
QY 352 GGCCAAAGGACACGCGTACCGTCTCC 378
Db 112 GlyGlnGlyThrLeuValThrValSer 120
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## RESULT 15

US-09-560-198A-2  
; Sequence 2, Application US/09560198A  
; Patent No. 6492497  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Julia E  
; APPLICANT: Leonard, Simon N  
; APPLICANT: Wilton, Alison J  
; APPLICANT: Braddock, Peta SH  
; APPLICANT: Du Fou, Sarah L  
; APPLICANT: McCafferty, John G  
; APPLICANT: Conroy, Louise A  
; APPLICANT: Tempest, Philip R  
; TITLE OF INVENTION: Specific binding members for TGFbeta1  
; FILE REFERENCE: 28111/35620A  
; CURRENT APPLICATION NUMBER: US/09/560,198A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/131,983  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-560-198A-2

## Alignment Scores:

Pred. No.: 5,41e-54 Length: 123  
Score: 546.00 Matches: 108  
Percent Similarity: 91.34% Conservative: 8  
Best Local Similarity: 85.04% Mismatches: 7  
Query Match: 78.45% Indels: 4  
DB: 4 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-560-198A-2 (1-123)

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QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGCTCAAGCTGGAGGCTCCCTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGACGCTCTGGATTCACTTCAGTAGCTATGACATGACATGCGGATCCGCGAGCT 120
Db 21 SerCyAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGGAGTGGGTGGGCAATTATCATATGATGAAGTAATAATCTAT 180
Db 41 ProGlyLyseGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerIleLysTyrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATCCAGAACAAGCGCTGTAT 240
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCTGAGAGCTGAGACACGCGTGTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArg---Thr 99
QY 301 GGGTGGGCGAGTGGCTGAGACCTACTACTACTACGATATGAGCGTGGGGCCAAAGG 360
Db 100 GlyGlyTyrSerGly-----TyrAspThrSerGlyValGlnLeuTrpGlyGlnGly 116
QY 361 ACCACGGTACCGTCTCTCA 381
Db 117 ThrThrValThrValSerSer 123
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Search completed: August 29, 2005, 11:08:08  
Job time : 23.3526 secs



## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	686	98.6	138	14	US-10-325-694-150	Sequence 150, Appl1
2	686	98.6	457	18	US-10-778-915-1	Sequence 1, Appl1
3	683	98.1	138	14	US-10-325-694-144	Sequence 144, Appl
4	612	87.9	127	17	US-10-706-689-22	Sequence 22, Appl
5	612	87.9	127	18	US-10-988-360-22	Sequence 22, Appl
6	608.5	87.4	124	15	US-10-371-942-80	Sequence 82, Appl
7	608	87.4	127	17	US-10-706-689-36	Sequence 36, Appl
8	608	87.4	127	18	US-10-968-360-36	Sequence 36, Appl
9	602	86.5	125	15	US-10-232-088-107	Sequence 107, Appl
10	601	86.4	123	15	US-10-292-088-116	Sequence 116, Appl
11	598.5	86.0	122	9	US-09-144-886-68	Sequence 68, Appl
12	598.5	86.0	122	16	US-10-632-706-65	Sequence 65, Appl
13	597.5	85.8	122	9	US-09-144-886-65	Sequence 65, Appl
14	597.5	85.8	122	16	US-10-632-706-66	Sequence 66, Appl
15	597.5	85.8	122	17	US-10-727-155-34	Sequence 34, Appl
16	597	85.5	123	15	US-10-292-088-115	Sequence 115, Appl
17	595.5	85.6	126	17	US-10-727-155-128	Sequence 128, Appl
18	595	85.5	123	15	US-10-292-088-117	Sequence 117, Appl
19	594.5	85.4	124	15	US-10-292-088-106	Sequence 106, Appl
20	591	84.9	451	14	US-10-153-382-17	Sequence 17, Appl
21	591	84.9	451	16	US-10-612-997-70	Sequence 70, Appl
22	591	84.9	451	16	US-10-776-649-10	Sequence 70, Appl
23	590	84.8	123	15	US-10-269-711-33	Sequence 43, Appl
24	590	84.8	123	16	US-10-664-109-35	Sequence 35, Appl
25	589.5	84.7	126	14	US-10-041-860-17	Sequence 17, Appl
26	589.5	84.7	126	14	US-10-041-860-25	Sequence 25, Appl
27	589.5	84.7	126	14	US-10-041-860-209	Sequence 209, Appl
28	589.5	84.7	126	14	US-10-041-860-210	Sequence 210, Appl
29	589.5	84.7	126	14	US-10-041-860-246	Sequence 246, Appl
30	589.5	84.7	126	14	US-10-041-860-282	Sequence 282, Appl
31	589.5	84.7	126	14	US-10-041-860-306	Sequence 306, Appl
32	589.5	84.7	126	16	US-10-665-383-14	Sequence 14, Appl
33	589.5	84.7	126	16	US-10-665-383-30	Sequence 30, Appl
34	589.5	84.7	123	17	US-10-727-155-254	Sequence 254, Appl
35	589.5	84.7	123	15	US-10-269-711-11	Sequence 11, Appl
36	587	84.3	123	15	US-10-269-711-23	Sequence 23, Appl
37	587	84.3	123	15	US-10-269-711-27	Sequence 27, Appl
38	587	84.3	123	15	US-10-269-711-31	Sequence 31, Appl
39	587	84.3	123	15	US-10-269-711-35	Sequence 35, Appl
40	587	84.3	123	16	US-10-684-109-11	Sequence 11, Appl
41	586	84.2	123	17	US-10-727-155-124	Sequence 124, Appl
42	586	84.2	252	10	US-09-880-748-1731	Sequence 1731, Appl
43	586	84.2	252	15	US-10-293-418-1731	Sequence 11, Appl
44	585.5	84.1	141	17	US-09-880-855-11	Sequence 11, Appl
45	585.5	84.1	249	10	US-09-880-748-512	Sequence 512, Appl

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? RESULT 1
? US-10-325-694-150
? Sequence 150. Application US/10325694
? Publication No. US20030148463A1
? GENERAL INFORMATION:
?
? APPLICANT: KUPFER, PETER
? APPLICANT: RADU, TOBIAS
? TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
? TITLE OF INVENTION: RECEPTORS AND USES THEREOF
? FILE REFERENCE: 38164000
? CURRENT APPLICATION NUMBER: US/10/325,694
? CURRENT FILING DATE: 2002-12-19
? PRIOR APPLICATION NUMBER: US/09/403,107
? PRIOR FILING DATE: 1999-10-14
? NUMBER OF SEQ ID NOS: 152
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 150
? LENGTH: 138
? TYPE: PR1
? ORGANISM: HUMAN
?

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US-10-325-694-150

Alignment Scores:

Pred. No.: 1,68e-61 Length: 138  
Score: 686.00 Matches: 126  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.21% Mismatches: 0  
Query Match: 98.56% Indels: 0  
DB: 14 Gaps: 0

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-10-325-694-150 (1-138)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGATCCAGAGGTCCCTGAGACTC 60  
Db 1 GluValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATGCACTGGTCCGCAAGCT 120  
Db 21 SerCyValAlaSerGlyPheThrPheSerSerTyGlyMetHisTrpValArgGlnAla 40  
QY 121 CCAGGCAAGGGCGCTGGAGTGGGTGGCGAGTATATCATATGAGTAATAATATCTAT 180  
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValAlleSerTyArgSpGlySerAsnLysTyTr 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAACGCTGTAT 240  
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80  
QY 241 CTGCAATGAACAACCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGATATG 300  
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTrCySalAlaYsAspMet 100  
QY 301 GGGTGGGCGAGTGGCTGGAGACCTTACTACTACGTATGACGCTGGGCGCAAGGG 360  
Db 101 GlyTrpGlySerGlyTrpArgProTyTrTyTrTyGlyMetCaspValIrrpGlyGlnGly 120  
QY 361 ACCACGGTCACCGTCTCTCA 381  
Db 121 ThrThrValThrValSerSer 127

RESULT 2

US-10-778-915-1  
; Sequence 1, Application US/10778915  
; Publication No. US20050180979A1  
; GENERAL INFORMATION:  
; APPLICANT: PETERS, MATTHEW  
; APPLICANT: LOCHER, MATTHIAS  
; APPLICANT: PRANG, NADJA  
; APPLICANT: QUADT, CORNELIA  
; TITLE OF INVENTION: Anti-EpCAM Immunoglobulins  
; FILE REFERENCE: DEBR.031US  
; CURRENT APPLICATION NUMBER: US/10/778,915  
; CURRENT FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 457  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-778-915-1

Alignment Scores:

Pred. No.: 2,09e-61 Length: 457  
Score: 686.00 Matches: 126  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.21% Mismatches: 0  
Query Match: 98.56% Indels: 0  
DB: 18 Gaps: 0

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-10-778-915-1 (1-457)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGATCCAGAGGTCCCTGAGACTC 60  
Db 1 GluValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATGCACTGGTCCGCAAGCT 120  
Db 21 SerCyValAlaSerGlyPheThrPheSerSerTyGlyMetHisTrpValArgGlnAla 40  
QY 121 CCAGGCAAGGGCGCTGGAGTGGGTGGCGAGTATATCATATGAGTAATAATATCTAT 180  
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValAlleSerTyArgSpGlySerAsnLysTyTr 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAACGCTGTAT 240  
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80  
QY 241 CTGCAATGAACAACCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGATATG 300  
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTrCySalAlaYsAspMet 100  
QY 301 GGGTGGGCGAGTGGCTGGAGACCTTACTACTACGTATGACGCTGGGCGCAAGGG 360  
Db 101 GlyTrpGlySerGlyTrpArgProTyTrTyTrTyGlyMetCaspValIrrpGlyGlnGly 120  
QY 361 ACCACGGTCACCGTCTCTCA 381  
Db 121 ThrThrValThrValSerSer 127

RESULT 3

US-10-325-694-144  
; Sequence 144, Application US/10325694  
; Publication No. US20030148463A1  
; GENERAL INFORMATION:  
; APPLICANT: KUPER, PETER  
; APPLICANT: RAUM, TOBIAS  
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN  
; FILE REFERENCE: 38164000  
; CURRENT APPLICATION NUMBER: US/10/325,694  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US/09/403,107  
; PRIOR FILING DATE: 1999-10-14  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 144  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-10-325-694-144

Alignment Scores:

Pred. No.: 3,41e-61 Length: 138  
Score: 683.00 Matches: 125  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.43% Mismatches: 0  
Query Match: 98.13% Indels: 0  
DB: 14 Gaps: 0

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-10-325-694-144 (1-138)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGATCCAGAGGTCCCTGAGACTC 60  
Db 1 GluValGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATGCACTGGTCCGCAAGCT 120  
Db 21 SerCyValAlaSerGlyPheThrPheSerSerTyGlyMetHisTrpValArgGlnAla 40  
QY 121 CCAGGCAAGGGCGCTGGAGTGGGTGGCGAGTATATCATATGAGTAATAATATCTAT 180  
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValAlleSerTyArgSpGlySerAsnLysTyTr 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTCAACCATCTCCAGAGACAATTCCAAGAACGCTGTAT 240

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Db 61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAGATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGATTACTGTGCGAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaIleLysAspMet 100
Qy 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACTACGATGAGAGCTTGGGGCCAGGG 360
Db 101 G1YTPG1YSERG1YTPARG1PROT1YTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTY 120
Qy 361 ACCAGGCTCAGCTCTCTCTCA 381
Db 121 ThrThrValThrValSerSer 127

RESULT 4
US-10-706-689-22
; Sequence 22, Application US/10706689
; Publication No. US20050100965A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wieleter, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BHC-085
; CURRENT APPLICATION NUMBER: US/10/706,689
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 22
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-689-22

Alignment Scores:
Pred. No.: 6,49e-54 Length: 127
Score: 612.00 Matches: 115
Percent Similarity: 94.53% Conservative: 6
Best Local Similarity: 89.84% Mismatches: 5
Query Match: 87.93% Indels: 2
Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-706-689-22 (1-127)
Qy 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCCAGCTGGAGGTCCTTGAGACTC 60
Db 1 ***ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCCGTGAGGCTCTGAGTTCAGCTTCAGTAGCTATGATGAGATGAGATTAATAATCTAT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerHisTyrGlyMetHisTyrValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGAGATTAATAATCTAT 180
Db 41 ProGlyysGlyLeuGlnTyrValAlaValIleSerTyrAspGlyArgAsnIleTyrTyr 60
Qy 181 GCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGACAAATTCAGAGACAGCTGTAT 240
Db 61 ValAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAGATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGATTACTGTGCGAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValPheTyrCysAlaArgGlnLys 100
Qy 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACTACTACGATGAGAGCTTGGGGCCAA 357
Db 101 Gly---GlySerGlyTyrProProPheTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyr 119
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Qy 358 GGGACCAAGCTCACCTCTCTCTCA 381
Db 120 GlyThrThrValThrValSerSer 127

RESULT 5
US-10-988-360-22
; Sequence 22, Application US/10988360
; Publication No. US20050147610A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wieleter, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BHC-0850S
; CURRENT APPLICATION NUMBER: US/10/988,360
; CURRENT FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 22
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-988-360-22

Alignment Scores:
Pred. No.: 6,49e-54 Length: 127
Score: 612.00 Matches: 115
Percent Similarity: 94.53% Conservative: 6
Best Local Similarity: 89.84% Mismatches: 5
Query Match: 87.93% Indels: 2
Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-988-360-22 (1-127)
Qy 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCCAGCTGGAGGTCCTTGAGACTC 60
Db 1 ***ValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy 61 TCCGTGACGCTCTGAGTTCAGCTTCAGTAGCTATGATGAGATGAGATTAATAATCTAT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerHisTyrGlyMetHisTyrValArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGTGGGTGGAGTATATCATATGATGAGAGATTAATAATCTAT 180
Db 41 ProGlyysGlyLeuGlnTyrValAlaValIleSerTyrAspGlyArgAsnIleTyrTyr 60
Qy 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAATTCAGAGACAGCTGTAT 240
Db 61 ValAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
Qy 241 CTGCAGATGAACAGCTGAGAGCTGAGAGACAGCGCTGTGATTACTGTGCGAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValPheTyrCysAlaArgGlnLys 100
Qy 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACTACTACTACGATGAGAGCTTGGGGCCAA 357
Db 101 Gly---GlySerGlyTyrProProPheTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyr 119
Qy 358 GGGACCAAGCTCACCTCTCTCTCA 381
Db 120 GlyThrThrValThrValSerSer 127

RESULT 6
US-10-371-942-82
; Sequence 82, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
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; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-371-942-82

Alignment Scores:
Pred. No.: 1.48e-53 Length: 124
Score: 608.50 Matches: 114
Percent Similarity: 94.49% Conservative: 6
Best Local Similarity: 89.76% Mismatches: 4
Query Match: 87.43% Indels: 3
DB: 15 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x US-10-371-942-82 (1-124)
QY 1 GAGGTGACAGTCTGCTCAGTCTGGGGAGGCGCTGCTCAGCTGGAGGTCCCTGAGACTTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyValrSerLeuArgLeu 20
QY 61 TCCTGTGACAGCTCTGGATTCACTTCAGTAGCTATGSCATGACGAGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyGlyMetHisTrpValAlaGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGAGTGCGGAGATTATGATGAAATTAATAACTAT 180
DB 41 ProGlyLyseGlyLeuGluTrpValAlaValIleSerTyAspGlySerAsnLysTrpTy 60
QY 181 GCAGACTCCGTGAGGGCCGATTCACCATCTCCAGAGCAATCCCAAGAACAGCTGTAT 240
DB 61 AlaAspSerValIysGlyArgPheThrIleSerTyAspAsnSerLysAsnThrLeuTy 80
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGGACACCGCTGTGTATTACTGTGCGAAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValIleTyCysAlaArgAspPhe 100
QY 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACTAGGATGAGAGCTTGGGGCCAGGG 360
DB 101 AspTyGlyAspSer-----TyTyTyTyTyGlyMetAspValTrpGlyGlnGly 117
QY 361 ACCAGGTCACCGTCTCCTCA 381
DB 118 ThrThrValThrValSerSer 124

RESULT 7
US-10-706-689-36
; Sequence 36, Application US/10706689
; Publication No. US20050100965A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wiele, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BBC-085
; CURRENT APPLICATION NUMBER: US/10/706,689
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 47
```

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; SEQ ID NO 36
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-706-689-36

Alignment Scores:
Pred. No.: 1.67e-53 Length: 127
Score: 608.00 Matches: 118
Percent Similarity: 94.53% Conservative: 3
Best Local Similarity: 92.19% Mismatches: 5
Query Match: 87.36% Indels: 2
DB: 17 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-706-689-36 (1-127)
QY 1 GAGGTGACAGTCTGCTCAGTCTGGGGAGGCGCTGCTCAGCTGGAGGTCCCTGAGACTTC 60
DB 1 ***ValGlnLeuValGlnSerGlyGlyValValGlnProGlyValrSerLeuArgLeu 20
QY 61 TCCTGTGACAGCTCTGGATTCACTTCAGTAGCTATGSCATGACGAGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerHisCysGlyMetHisTrpValAlaGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGAGTGCGGAGATTATGATGAAATTAATAACTAT 180
DB 41 ProGlyLyseGlyLeuGluTrpValAlaValIleSerTyAspGlySerAsnLysTrpTy 60
QY 181 GCAGACTCCGTGAGGGCCGATTCACCATCTCCAGAGCAATCCCAAGAACAGCTGTAT 240
DB 61 AlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80
QY 241 CTGCAATGAAACAGCTGAGAGCTGAGGACACCGCTGTGTATTACTGTGCGAAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValIleTyCysAlaArgAspHis 100
QY 301 GGGTGGGGCAGTGGCTGGAGACCC--TACTACTACTAGGATGAGAGCTTGGGGCCAA 357
DB 101 Gly---GlySerGlySerProProPheTyTyTyTyTyGlyMetAspValTrpGlyGln 119
QY 358 GGGACCAAGCTACCGTCTCCTCA 381
DB 120 GlyThrThrValThrValSerSer 127

RESULT 8
US-10-988-360-36
; Sequence 36, Application US/10988360
; Publication No. US20050147610A1
; GENERAL INFORMATION:
; APPLICANT: Ghayur, Tariq
; APPLICANT: Labkovsky, Boris
; APPLICANT: Voss, Jeffrey
; APPLICANT: Green, Larry
; APPLICANT: Babcock, John
; APPLICANT: Jia, Xiao-chi
; APPLICANT: Wiele, James
; APPLICANT: Kang, Paul
; APPLICANT: Hegberg, Brad
; TITLE OF INVENTION: IL-18 Binding Proteins
; FILE REFERENCE: BBC-085US
; CURRENT APPLICATION NUMBER: US/10/988,360
; CURRENT FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 36
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-988-360-36

Alignment Scores:
Pred. No.: 1.67e-53 Length: 127
Score: 608.00 Matches: 118
Percent Similarity: 94.53% Conservative: 3
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Qy 1 GAGGTGACGCTGCTCCAGTCTTGGGGGAGGCGTGGTTCACGCTCGAGAGGTCCCTTGAAGATC 60  
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
Db 1 GlnValGlnLeuValGlnSerArgIysGlyValValGlnProGlyArgSerLeuArgLeu 20  
Qy 61 TCCCTGACACGCTCTGGATTACACCTTCAGTACGATATGCGATGCACCTGGGTCCGCGAGGCT 120

Qy	1	GAAGTGCACCTCTCGAGTCTGGGGGAGAGCGCTGGTTCACAGCTCGGAGAGTCCCTGAGATC	60
	...	...	...
Db	1	GlnValGlnLeuValGlnSerGlyGlyGlyValValGlnProGlyArgSerSerLeuArgLeu	20
Qy	61	TCCTGTGCAGCCTCTGGATTCACCTTCAGTACGATGGCATGCATGGGTCCGCAGAGCT	120
Db	21	SerCysAlaIleSerGlyPheThrPheSerSerTyrGlyMetHisTyrValArgGlnAla	40
Qy	121	CCAGGCAAGGGGCTCGAATGGGTGGCAATTATCATATGATGGAACTAATAATCTAT	180
Db	41	ProGlyLysGlyLeuGluTrrPValAlaValIleSerTyrAspGlySerAsnLysTyr	60
Qy	181	GCAGACTCCGTAAAGGGCCGATACCACTTCACGAGACAAATTCAAAGAACAGCTGTAT	240
Db	61	AlaAspSerValLysGlyLysArgPheThrIleSerTyrGlnAsnSerLysPheAsnTrpLeuTyr	80

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QY 241 CTGCAATGAAACGCTGAGAGCTGAGACACGCGTGTGTAATTACTGTGCGAAGATATG 300
|||
Db 81 LeuGIlnMetAsnSerLeuAlaGluAspThrAlaValTyrTyrCysAlaArgAsp---- 99
QY 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACGATTAGGACGCTGGGGCCCAAGG 360
|||
Db 100 ---TyrGlyAspTyrTyr-----TyrTyrTyrTyrGlyMetAspValTyrGlyGlnGly 116
QY 361 ACCAGCGTCAACCGTCTCCCTCA 381
|||
Db 117 ThrThrValThrValSerSer 123

RESULT 11
US-09-144-886-68
; Sequence 68, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-68

Alignment Scores:
Pred. No.: 1,56e-52 Length: 122
Score: 598.50 Matches: 115
Percent Similarity: 92.13% Conservative: 2
Best Local Similarity: 90.55% Mismatches: 5
Query Match: 85.99% Indels: 5
Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-09-144-886-68 (1-122)
QY 1 GAGGTGCACTGCTCCAGTGTGGGGGAGCGCTGTCACGCTGGAGGTCCTCCAGACTC 60
|||
Db 1 GluValGlnLeuGlnGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGCAAGCTCTGGATTCACTTCAGTAGCTATGCGATGCGAGTGGTCCGCAAGCT 120
|||
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAGTAATAATATAT 180
|||
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60
QY 181 GCGAGTCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAATTCGAAGAACAGCTGTAT 240
|||
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAAACGCTGAGAGCTGAGACACGCGTGTGTAATTACTGTGCGAAGATATG 300
|||
Db 81 LeuGIlnMetAsnSerLeuAlaGluAspThrAlaValTyrTyrCysAlaArgAsp---- 99
QY 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACGATTAGGACGCTGGGGCCCAAGG 360
|||
Db 100 ---TrpSerGlnGly-----TyrTyrTyrTyrGlyMetAspValTyrGlyGlnGly 115
QY 361 ACCAGCGTCAACCGTCTCCCTCA 381
|||
Db 116 ThrThrValThrValSerSer 122
```

```
RESULT 12
US-10-632-706-65
; Sequence 65, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 4077-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-65

Alignment Scores:
Pred. No.: 1,56e-52 Length: 122
Score: 598.50 Matches: 115
Percent Similarity: 92.13% Conservative: 2
Best Local Similarity: 90.55% Mismatches: 5
Query Match: 85.99% Indels: 5
Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x US-10-632-706-65 (1-122)
QY 1 GAGGTGCACTGCTCCAGTGTGGGGGAGCGCTGTCACGCTGGAGGTCCTCCAGACTC 60
|||
Db 1 GluValGlnLeuGlnGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
QY 61 TCCTGTGCAAGCTCTGGATTCACTTCAGTAGCTATGCGATGCGAGTGGTCCGCAAGCT 120
|||
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetHisTrpValArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGTTATATCATATGATGAAGTAATAATATAT 180
|||
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60
QY 181 GCGAGTCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAATTCGAAGAACAGCTGTAT 240
|||
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAAACGCTGAGAGCTGAGACACGCGTGTGTAATTACTGTGCGAAGATATG 300
|||
Db 81 LeuGIlnMetAsnSerLeuAlaGluAspThrAlaValTyrTyrCysAlaArgAsp--- 99
QY 301 GGGTGGGGGAGTGGCTGGAGACCCCTACTACTACGATTAGGACGCTGGGGCCCAAGG 360
|||
Db 100 ---TrpSerGlnGly-----TyrTyrTyrTyrGlyMetAspValTyrGlyGlnGly 115
QY 361 ACCAGCGTCAACCGTCTCCCTCA 381
|||
Db 116 ThrThrValThrValSerSer 122

RESULT 13
US-09-144-886-69
; Sequence 69, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: Botulinum Neurotoxins
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FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 69  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-69

Alignment Scores:  
Pred. No.: 1,98e-52 Length: 122  
Score: 597.50 Matches: 113  
Percent Similarity: 92.91% Conservative: 5  
Best Local Similarity: 88.98% Mismatches: 4  
Query Match: 85.85% Indels: 5  
DB: 9 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-09-144-886-69 (1-122)

QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGGCTCCCTGAGACTC 60  
DB 1 GlnIleGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCTGTGACGCTCTGATTCACCTTCAGTAGCTAGCATGACATGGGTCGCCAGGCT 120  
DB 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyraIaMetHisIstPValArgGlnIa 40  
QY 121 CCAGCAAGGGGCTGAGAGTGGGTGGCACTTATATCATATGATGAAATTAATTAATCAT 180  
DB 41 ProGlyLysGlyLeuGlnIstPValAlaValIleSerTyraSpGlySerAsnLysTyx 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGACAGCTGAT 240  
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyx 80  
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAGATATG 300  
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyxTyxTyxAlaArgAsp--- 99  
QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATGAGAGCTGTGGGGCCAGGG 360  
DB 100 ---TtpSerGlnGly-----TyxTyxTyxTyxGlyMetAspValIstPValGlnGly 115  
QY 361 ACCAGGTCACCGTCTCTCA 381  
DB 116 ThrThrValIleValSerSer 122

RESULT 14  
US-10-632-706-66  
Sequence 66, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: Patent Version 3.2  
SEQ ID NO 66  
LENGTH: 122  
TYPE: PRT

ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody  
US-10-632-706-66

Alignment Scores:  
Pred. No.: 1,98e-52 Length: 122  
Score: 597.50 Matches: 113  
Percent Similarity: 92.91% Conservative: 5  
Best Local Similarity: 88.98% Mismatches: 4  
Query Match: 85.85% Indels: 5  
DB: 16 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x US-10-632-706-66 (1-122)

QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGCTCCAGCTGGAGGCTCCCTGAGACTC 60  
DB 1 GlnIleGlnLeuLeuGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCTGTGACGCTCTGATTCACCTTCAGTAGCTAGCATGACATGGGTCGCCAGGCT 120  
DB 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyraIaMetHisIstPValArgGlnIa 40  
QY 121 CCAGCAAGGGGCTGAGAGTGGGTGGCACTTATATCATATGATGAAATTAATTAATCAT 180  
DB 41 ProGlyLysGlyLeuGlnIstPValAlaValIleSerTyraSpGlySerAsnLysTyx 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGCAATTCAGAGACAGCTGAT 240  
DB 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyx 80  
QY 241 CTGCAATGAACAGCTGAGAGCTGAGAGACAGGCTGTGATTACTGTGCGAAGATATG 300  
DB 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyxTyxTyxAlaArgAsp--- 99  
QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATGAGAGCTGTGGGGCCAGGG 360  
DB 100 ---TtpSerGlnGly-----TyxTyxTyxTyxGlyMetAspValIstPValGlnGly 115  
QY 361 ACCAGGTCACCGTCTCTCA 381  
DB 116 ThrThrValIleValSerSer 122

RESULT 15  
US-10-727-155-34  
Sequence 34, Application US/10727155  
Publication No. US20050049402A1  
GENERAL INFORMATION:  
APPLICANT: John S. Babcock  
APPLICANT: Jaapal S. Kang  
APPLICANT: Orlit Foord  
APPLICANT: Larry Green  
APPLICANT: Xiao Feng  
APPLICANT: Scott Klakamp  
APPLICANT: Mary Haak-Frendescho  
APPLICANT: Palaniswami Rathnaswami  
APPLICANT: Craig Pigott  
APPLICANT: Meina Liang  
APPLICANT: Rozanne Lee  
APPLICANT: Kathy Manchuliencho  
APPLICANT: Raffaela Faggioni  
APPLICANT: Giorgio Senaldi  
APPLICANT: Qiaojuan Jane Su  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
FILE REFERENCE: AGENIX.073A  
CURRENT APPLICATION NUMBER: US/10/727,155  
CURRENT FILING DATE: 2003-12-02  
PRIOR APPLICATION NUMBER: 60/430729  
PRIOR FILING DATE: 2002-12-02  
NUMBER OF SEQ ID NOS: 320  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 34

; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-34

## Alignment Scores:

Pred. No.:	1.98e-52	Length:	122
Score:	597.50	Matches:	114
Percent Similarity:	92.91%	Conservative:	4
Best Local Similarity:	89.76%	Mismatches:	5
Query Match:	85.85%	Indels:	2
DB:	17	Gaps:	2

US-09-403-107-143\_copy\_1\_381 (1-381) x US-10-727-155-34 (1-122)

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QY      1 GAAGTGCAGCTGCTCGAGTCTGGGGAGGCTGTCACGCTGGGAGGTCCCTGAGACTC 60
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

QY      61 TCCTGTGCAGGCTCTGGATTCACTTCAGTAGCTATGGCATGGAGTGGGTCCGCCAGGCT 120
        |||
Db      21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40

QY      121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGAAATAATAATATCTAT 180
        |||
Db      41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60

QY      181 GCAGACTCCGCTGAAGGCCGATTCACTATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
        |||
Db      61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

QY      241 CTGCAATGTAACAGCTGAGAGCTGAGAGACACGGCTGTGATTACTGTGGCAAAAGATATG 300
        |||
Db      81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaArgAspGln 100

QY      301 GGGTGGGGCAGTGGCTGGAGACCCCTACTACTACTACGTATGAGACGCTTGGGGCCAAAGG 360
        |||
Db      101 -----AspAsnTrpAsn-----TyrTyrTyrGlyMetAspValTrpGlyGlnGly 115

QY      361 ACCACGGTCAACGCTTCTCTCA 381
        |||
Db      116 ThrThrValThrValSerSer 122
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Search completed: August 29, 2005, 11:30:07  
Job time : 358.577 secs



1 GAGTGCAGCTGCTCGAGTCTGGGGGAGGCTGTGTCAGCTGGAGGTCCCTGAGACTC 60

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Dh      1 GluValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy      61 TCCTGTGCAGCCTCTGTGATTCACCTTCAGTACGTAAGCATGACATGGGTCCGCCAGGCT 120
Db      21 SerCysAlaIaIaSerGlyPheThrPheSerSerGlyMetHisrTrpValArgGlnAla 40
Qy      121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATATGAAAGTAAATAACTAT 180
Db      41 ProGlyLysGlyLeuGlnUtrpValAlaValIleTrpTyrAspIlySerLeuLysrTrpTyr 60
Qy      181 GCAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTAT 240
Db      61 AlaAspSerValIlySerGlyArgPheThrIleSerArgAspAsnSerIlysaThrLeuTyr 80
Qy      241 CTGCAAAATGAACGCTGAGAGAGCTGAGAGACACGGCTGTGTATTAATGCGAAAGATATG 300
Db      81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValrTrpCysAlaArgAspAsn 100
Qy      301 GGGTGG-----GGACGTGGCTGGAGACCTACTACTACTACGTATGACGTCGGGCG 354
Db      101 TyTrpTyrAspSerSerGlyrTrpTyr--TyTrpTyrTrpGlyMetAspValTrpGly 119
Qy      355 CAAGGACCAACGCTGACCGTCTCTCTCA 381
Db      120 GlnGlyThrThrValThrValSerSer 128

RESULT 2
E36005
Ig heavy chain V region (M72) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: E36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: E36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-122 <SCH>
A/Cross-references: GB:M34030
C/Genetics:
A/Gene: GDB:IGH@; IGHV1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterocyclamer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:      1,46e-47      length:      122
Score:          585.50      Matches:      113
Percent Similarity: 92.13%      Conservative: 4
Best Local Similarity: 88.98%      Mismatches: 5
Query Match:    84.12%      Indels:      5
                        Gaps:      2
US-09-403-107-143_COPY_1_381 (1-381) x E36005 (1-122)

Qy      1 GAGGTGCAGCTGCTCGAGTCTGGGGAGGCGTGGTCCAGGCTCGGAGGTCCTGAGACTC 60
Db      1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20
Qy      61 TCCTGTGCAGCCTCTGTGATTCACCTTCAGTACGTAAGCATGACATGGGTCCGCCAGGCT 120
Db      21 SerCysAlaIaIaSerGlyPheThrPheSerSerGlyMetHisrTrpValArgGlnAla 40
Qy      121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATATGAAAGTAAATAACTAT 180
Db      41 ProGlyLysGlyLeuGlnUtrpValAlaValIleSerTrpAspIlySerLeuLysrTrpTyr 60
Qy      181 GCAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTAT 240
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Dh      61 AlaAspSerValIlySerGlyArgPheThrIleSerArgAspAsnSerIlysaThrLeuTyr 80
Qy      241 CTGCAAAATGAACGCTGAGAGAGCTGAGAGACAGGCGTGTATTAATGCGAAAGATATG 300
Db      81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValrTrpCysAlaArgAspAsn 100
Qy      301 GGGTGGGAGAGGCTGGAGACCTACTACTACTACGTATGAGAGCTGGGGCCAGAGG 360
Db      101 ---HisSerSerSerTrp-----TyTrpGlyMetAspValTrpGlyGlnGly 115
Qy      361 ACCAGCGTCACCGTCTCTCA 381
Db      116 ThrThrValThrValSerSer 122

RESULT 3
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C/Accession: I37780; S25474
R/Demaison, C.; Chastagner, P.; These, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A/Title: Somatic diversification in the heavy chain variable region genes expressed by h
A/Reference number: A36876; MUID:94119917; PMID:8290556
A/Accession: I37780
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-147 <RES>
A/Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/28-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:      2,79e-47      length:      147
Score:          582.50      Matches:      113
Percent Similarity: 89.76%      Conservative: 1
Best Local Similarity: 88.98%      Mismatches: 10
Query Match:    83.69%      Indels:      3
                        Gaps:      1
US-09-403-107-143_COPY_1_381 (1-381) x I37780 (1-147)

Qy      1 GAGGTGCAGCTGCTCGAGTCTGGGGAGGCGTGGTCCAGGCTCGGAGGTCCTGAGACTC 60
Db      14 GluValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 33
Qy      61 TCCTGTGCAGCCTCTGTGATTCACCTTCAGTACGTAAGCATGACATGGGTCCGCCAGGCT 120
Db      34 SerCysAlaIaIaSerGlyPheThrPheSerSerGlyMetHisrTrpValArgGlnAla 53
Qy      121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATATGAAAGTAAATAACTAT 180
Db      54 ProGlyLysGlyLeuGlnUtrpValAlaValIleSerTrpAspIlySerLeuLysrTrpTyr 73
Qy      181 GCAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAAACACGCTGTAT 240
Db      74 AlaAspSerValIlySerGlyArgPheThrIleSerArgAspAsnSerIlysaThrLeuTyr 93
Qy      241 CTGCAAAATGAACGCTGAGAGAGCTGAGAGACACGGCTGTGTATTAATGCGAAAGATATG 300
Db      94 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValrTrpCysAlaArgAspAsn 112
Qy      301 GGGTGGGAGAGGCTGGAGACCTACTACTACTACGTATGAGAGCTGGGGCCAGAGG 360
Db      113 -----GlyGlnGlyTrpGlyLeuTrpTyrTrpTyrGlyMetAspValTrpGlyGlnGly 130
Qy      361 ACCAGCGTCACCGTCTCTCA 381
Db      131 ThrThrValThrValSerSer 137

RESULT 4
S31119
Ig heavy chain - human
```

Alignment Scores: 2.78e-46 Length: 123  
 Pred. No.: 572.00 Matches: 111  
 Score: 90.55% Conservative: 4  
 Percent Similarity: 87.40% Mismatches: 8  
 Best Local Similarity: 82.18% Indels: 4  
 Query Match: 2 Gaps: 2  
 DB: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x S38493 (1-123)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGGAGGCTGTCCAGCTGGAGTCCCTGAGACTC 60  
 Db 1 GlnValGlnLeuGlnLeuSerGlyGlyValValGlnProGlyArgSerLeuSerLeu 20  
 QY 61 TCCTGTGACGCTCTGGAATTACCTTCAGTAAGCTATGAGACATCGGATCCGACGGCT 120  
 Db 21 SerCysAlaIleSerGlyPheThrPheSerSerTyAlaMetHisThrValArgGlnAla 40  
 QY 121 CCAGGCGAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGAGAGTAAATATCTAT 180  
 Db 41 ProGlyLysPheLysLeuThrProValAlaValIleSerTyAspGlySerAsnLysTyTy 60  
 QY 181 GCAGACTCCGTGAAAGGGCGGATTCAACATCTCCAGAGAAATTCCGAAGAACCGCTGAT 240  
 Db 61 AlaAspSerValIleGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80  
 QY 241 CTCGAATGAACAGCTGTGAGAGCTGAGACACAGCGCTGTATTAATCTGTGCGAAGATATG 300  
 Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTyTyCysAlaArgAlaArg 100  
 QY 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACTACGTATGAGCGTCTGGGGCCAGGG 360  
 Db 101 -----SerAsnTrpAsn---TyTyTyTyTyTyTyTyMetAspValTrpGlyLysGly 116  
 QY 361 ACCACGGTCACCGCTCCCTCA 381  
 Db 117 ThrThrValThrValSerSer 123

RESULT 6  
 S19666  
 Ig heavy chain V region (VH3DJH4) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Jan-1993 #Sequence\_revision 22-Jan-1993 #ext\_change 20-Jun-2000  
 C/Accession: S19666  
 R/Mark: J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
 A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage  
 A/Reference number: S19663; M0ID:92085276; PMID:1748994  
 A/Residues: 1-121 <EMBL>  
 A/Molecule type: mRNA  
 A/Cross-references: EMBL:X61646; NID:g37688; P1D:CA43827.1; P1D:g1335369  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores: 1.99e-45 Length: 121  
 Pred. No.: 563.00 Matches: 110  
 Percent Similarity: 91.34% Conservative: 6  
 Best Local Similarity: 86.61% Mismatches: 5  
 Query Match: 80.89% Indels: 6  
 DB: 2 Gaps: 3

US-09-403-107-143\_COPY\_1\_381 (1-381) x S19666 (1-121)

QY 1 GAGGTGACGCTGCTCGAGTCTGGGGGAGGCTGTCCAGCTGGAGTCCCTGAGACTC 60  
 Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20  
 QY 61 TCCTGTGACGCTCTGGAATTACCTTCAGTAAGCTATGAGACATCGGATCCGACGGCT 120  
 Db 21 SerCysAlaIleSerGlyPheThrPheSerSerTyAlaMetHisThrValArgGlnAla 40  
 QY 121 CCAGGCGAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGAGAGTAAATATCTAT 180  
 Db 41 ProGlyLysPheLysLeuThrProValAlaValIleSerTyAspGlySerAsnLysTyTy 60  
 QY 181 GCAGACTCCGTGAAAGGGCGGATTCAACATCTCCAGAGAAATTCCGAAGAACCGCTGAT 240  
 Db 61 AlaAspSerValIleGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80  
 QY 241 CTCGAATGAACAGCTGTGAGAGCTGAGACACAGCGCTGTATTAATCTGTGCGAAGATATG 300  
 Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTyTyCysAlaArgAlaArg 100  
 QY 301 GGGTGGGGCAGTGGCTGGAGACCTTACTACTACTACGTATGAGCGTCTGGGGCCAGGG 360  
 Db 101 -----SerAsnTrpAsn---TyTyTyTyTyTyTyTyMetAspValTrpGlyLysGly 116  
 QY 361 ACCACGGTCACCGCTCCCTCA 381  
 Db 117 ThrThrValThrValSerSer 123

```
Dh 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrclywchIstRValaArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGAGTGGGCTGAGTTATATCATATGAGTAAATACTAT 180
Db 41 ProGlyysGlyLeuGluTrpValaIaValIleSerTyrsApGlySerAenlystYrTy 60
Qy 181 GCAGACTCCGTAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTAT 240
Db 61 AlaAspSerValIysGlyArgPheThrIleSerThrGspAsnSerlysaSnThrLeuTy 80
Qy 241 CTGCAATGAACAGCCTGAGAGAGTGAAGACAGCGCTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValIlyrTyrcysAlaIys---Thr 99
Qy 301 GGGTGGGCGAGTGGCTGAGACACCTTACTACTACGCTATGACGCTGGGCGCAAGGG 360
Db 100 GlyTyrSerSerGlyTrpGly-----TyrPhe-----AspTyrTrpGlyGlnGly 114
Qy 361 ACCACGGTCACCGTCTCTCTCA 381
Db 115 ThrLeuValThrValSerSer 121
```

## RESULT 7

S31603  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31603  
R/CuiSnier, A.M.; Gauchier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31603  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-132 <CUI>  
A/Cross-references: EMBL:Z4168; NID:G30999; PIDN:CAA78537.1; PID:G31000  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:30-113/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2,47e-45 Length: 132  
Score: 562.00 Matches: 108  
Percent Similarity: 89.76% Conservative: 6  
Best Local Similarity: 85.04% Mismatches: 3  
Query Match: 80.75% Indels: 10  
Gaps: 2  
US-09-403-107-143\_copy\_1\_381 (1-381) x S31603 (1-132)

```
Qy 1 GAGGTGACGTGCTCCGAGTCTGGGGAGGCGCTGCTCCAGCCTGGAGAGTCCCTGAGACTC 60
Db 16 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyAspSerLeuArgLeu 35
Qy 61 TCGTGTGACGCTCTGTGATTCACCTTCAGTAGTATGAGCATGCGTGGTCCGCGAGCT 120
Db 36 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrclywchIstRValaArgGlnAla 55
Qy 121 CCAGGCAAGGGGCTGAGAGTGGGCTGAGTTATATCATATGAGTAAATACTAT 180
Db 56 ProGlyysGlyLeuGluTrpValaIaValIleSerTyrsApGlySerAenlystYrTy 75
Qy 181 GCAGACTCCGTAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTAT 240
Db 76 AlaAspSerValIysGlyArgPheThrIleSerThrGspAsnSerlysaSnThrLeuTy 95
Qy 241 CTGCAATGAACAGCCTGAGAGAGTGAAGACAGCGCTGTATTACTGTGCGAAAGATATG 300
Db 96 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValIlyrTyrcysAlaIysApRleu 115
Qy 301 GGGTGGGCGAGTGGCTGAGACACCTTACTACTACGCTATGACGCTGGGCGCAAGGG 360
Db 301 GGGTGGGCGAGTGGCTGAGACACCTTACTACTACGCTATGACGCTGGGCGCAAGGG 360
```

```
Dh 116 -----PheTyrcTyPhe-----AspTyrTrpGlyGlnGly 125
Qy 361 ACCACGGTCACCGTCTCTCTCA 381
Db 126 ThrLeuValThrValSerSer 132
```

## RESULT 8

S46390  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S46390  
R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A/Reference number: S46390, M01D:94254092, PMID:8196048  
A/Accession: S46390  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-114 <FIG>  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-114 <FIG>  
A/Cross-references: EMBL:Z31686; NID:G509782; PIDN:CAA83491.1; PID:G1335143  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1,59e-44 Length: 114  
Score: 553.50 Matches: 108  
Percent Similarity: 87.40% Conservative: 3  
Best Local Similarity: 85.04% Mismatches: 3  
Query Match: 79.53% Indels: 13  
Gaps: 2  
US-09-403-107-143\_copy\_1\_381 (1-381) x S46390 (1-114)

```
Qy 1 GAGGTGACGTGCTCCGAGTCTGGGGAGGCGCTGCTCCAGCCTGGAGAGTCCCTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyAspSerLeuArgLeu 20
Qy 61 TCGTGTGACGCTCTGTGATTCACCTTCAGTAGTATGAGCATGCGTGGTCCGCGAGCT 120
Db 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTyrclywchIstRValaArgGlnAla 40
Qy 121 CCAGGCAAGGGGCTGAGAGTGGGCTGAGTTATATCATATGAGTAAATACTAT 180
Db 41 ProGlyysGlyLeuGluTrpValaIaValIleSerTyrsApGlySerAenlystYrTy 60
Qy 181 GCAGACTCCGTAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAGACGCTGTAT 240
Db 61 AlaAspSerValIysGlyArgPheThrIleSerThrGspAsnSerlysaSnThrLeuTy 80
Qy 241 CTGCAATGAACAGCCTGAGAGAGTGAAGACAGCGCTGTATTACTGTGCGAAAGATATG 300
Db 81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValIlyrTyrcysAlaIysApRleu 99
Qy 301 GGGTGGGCGAGTGGCTGAGACACCTTACTACTACGCTATGAGTAAATACTAT 360
Db 100 ---TrrpGly-----AspTyrTrpGlyGlnGly 107
Qy 361 ACCACGGTCACCGTCTCTCTCA 381
Db 108 ThrLeuValThrValSerSer 114
```

RESULT 9  
S31116  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C/Accession: S31116  
R/Kaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, E.; J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme  
A/Reference number: S31104; M01D:92111633; PMID:1730252

A:Accession: S31116  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-118 <RNA>  
A:Cross-references: UNIPROT:O8WUK1; EMBL:X62966  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
P:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.59e-44 Length: 118  
Score: 553.50 Matches: 107  
Percent Similarity: 88.19% Conservative: 5  
Best Local Similarity: 84.25% Mismatches: 6  
Query Match: 79.53% Indels: 9  
DB: 2 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x S31116 (1-118)

```
OY 1 GAGGTGACGCTGCTGAGTCTGGGGAGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

OY 61 TCCTGTGACGCTCTGATTCACCTTCAGTAGCTATGCGATGCACTGGGCGCAGGCT 120
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 21 SerCysAlaIaSerGlyPheThrPheSerSerTyGlyMetHisTrpValArgGlnIla 40

OY 121 CCAGGCAAGGGGCTGAGTGGGTGGGTCAGTTATCATATGATGAGTAATAATACTAT 180
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyraSerGlySerAsnLysTyTr 60

OY 181 GCAGACTCTCGTGAAGGGCCGATTCCACATCTCCAGAGCAATTCGAAGAACGCTGAT 240
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80

OY 241 CTGCAAAATGAACAGCCTGAGAGCTGAGACACGCGTGATTTACTGTGCGAAAGATATG 300
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 81 LeuGlnMetCysSerLeuArgAlaGlnAspThrAlaValTyTrCysAlaThrAspGly 100

OY 301 GGGTGGGCGCAGTGGCTGAGACCCCTACTACTACGTATGAGACGTCGGGCGCAAGG 360
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 101 GlyLysAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 111
   -----PheAspIleTrpGlyGlnGly 111

OY 361 ACCACGCTGACCGTCTCTCTCA 381
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 112 ThrMetValThrValSerSer 118
```

## RESULT 10

G36005  
Ig heavy chain V region (M74) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 09-Jul-2004  
C:Accession: G36005  
R:Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A66005; MUID:90349571; PMID:2117273  
A:Accession: G36005  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-121 <SCH>  
A:Cross-references: UNIPROT:O8WUK1; GB:M34031  
C:Genetics:  
A:Gene: GDB:IGH@; IGHDI1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
P:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2.74e-44 Length: 121

Score: 551.00 Matches: 108  
Percent Similarity: 85.38% Conservative: 3  
Best Local Similarity: 83.08% Mismatches: 7  
Query Match: 79.17% Indels: 12  
DB: 2 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x G36005 (1-121)

```
OY 1 GAGGTGACGCTGCTGAGTCTGGGGAGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

OY 61 TCCTGTGACGCTCTGATTCACCTTCAGTAGCTATGCGATGCACTGGGCGCAGGCT 120
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 21 SerCysAlaIaSerGlyPheThrPheSerSerTyraIleMetHisTrpValArgGlnIla 40

OY 121 CCAGGCAAGGGGCTGAGTGGGTGGGTCAGTTATCATATGATGAGTAATAATACTAT 180
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyraSerGlySerAsnLysTyTr 60

OY 181 GCAGACTCTCGTGAAGGGCCGATTCCACATCTCCAGAGCAATTCGAAGAACGCTGAT 240
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTy 80

OY 241 CTGCAAAATGAACAGCCTGAGAGCTGAGACACGCGTGATTTACTGTGCG----- 291
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 81 LeuGlnMetCysSerLeuArgAlaGlnAspThrAlaValTyTrCysAlaThrAspGly 100

OY 292 AAAGATATGAGGGGCTGAGTGGGTGGGTCAGTACTACTACTACGTATGAGACGCTG 351
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 101 LysAspTrpGlyTrpAlaLeu-----PheAspTyTrp 111

OY 352 GGGCAAGGAGACACGCTGACCGTCTCTCA 381
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 112 GlyGlnGlyThrLeuValThrValSerSer 121
```

## RESULT 11

G31117  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31117  
R:Raaphorst, P.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31117  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-122 <RNA>  
A:Cross-references: EMBL:X62967  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
P:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 4.73e-44 Length: 122  
Score: 548.50 Matches: 106  
Percent Similarity: 87.40% Conservative: 5  
Best Local Similarity: 83.46% Mismatches: 11  
Query Match: 78.81% Indels: 5  
DB: 2 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x S31117 (1-122)

```
OY 1 GAGGTGACGCTGCTGAGTCTGGGGAGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 20

OY 61 TCCTGTGACGCTCTGATTCACCTTCAGTAGCTATGCGATGCACTGGGCGCAGGCT 120
   ||::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 21 SerCysAlaIaSerGlyPheThrPheSerSerTyGlyMetHisTrpValArgGlnIla 40
```



R:Kishimoto, T  
submitted to the EMBL Data Library, March 1989  
A:Reference number: S05270  
A:Accession: S05271  
A:Molecule type: mRNA  
A:Residues: 1-160 <K1s1>  
A:Cross-references: UNIPROT:096BB9; EMBL:X14584  
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.  
Nucleic Acids Res. 17, 4385, 1989  
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of  
A:Reference number: S04601; MUID:89296497; PMID:2500644  
A:Accession: S04602  
A:Molecule type: mRNA  
A:Residues: 1-144 <K1S2>  
A:Cross-references: EMBL:X14584  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterodimer; immunoglobulin  
P:1-19/Domains: signal sequence #status predicted <Sig>  
F:20-160/Product: Ig heavy chain (fragment) #status predicted <Mat>  
P:34-117/Domains: immunoglobulin homology <IM>

Alignment Scores:  
Pred. No.: 1,94e-43 Length: 160  
Score: 542.00 Matches: 107  
Percent Similarity: 87.40% Conservative: 4  
Best Local Similarity: 84.25% Mismatches: 14  
Query Match: 77.87% Indels: 2  
DB: Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x S05271 (1-160)

OY 1 GAGGTGACAGCTCTGAGTCTGGGGAGGCTGTCACGCTGGAGAGTCCCTGAGACTC 60  
DB 20 GUVValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39  
OY 61 TCGGTGAGAGCTCTGAGTACCTTCAGTCACTTACGACTATGAGATCAGTCCGCAAGCT 120  
DB 40 SerCysAlaAlaSerGlyPheThrPheSerThrTyrAlaMetSerTyrValArgGlnAla 59  
OY 121 CCAGGCAAGGGCTGAGTGGGTGAGCAGTATATGATGATGAGTAAGTAAATACTAT 180  
DB 60 ProGlyLysGlyLeuGlnTyrPalaSerAlaIleSerGlySerGlyGlySerThrTyr 79  
OY 181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAATCCAGAAACGCTGTAT 240  
DB 80 AlaAspSerValIleGlyAlaPheThrIleSerAlaGAspAsnSerLysAsnThrLeuTyr 99  
OY 241 CTGCAAAAGACAGCTGAGCTGAGACAGCGCTGCTATTAATCTGCCAAAGATATG 300  
DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValIleTyrCysAlaIleValAla 119  
OY 301 GGGTGGGAGCAGTGGTGAAGACCTTACTACTACTAGGATGAGAGTGGGGCCAGGG 360  
DB 120 -----ValArgGlyValIleSerTyrTyrTyrGlyMetAspValTyrGlyGln 137  
OY 361 ACCAGGTCACCGTCTCTCA 381  
DB 138 ThrThrValThrValSerSer 144

RESULT 15  
S31674  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31674  
R:Guisbater, A.M.; Gauchier, L.; Boudil, L.; Fougereau, M.; Tonnelie, C.  
Submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31674  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CU>

A:Cross-references: EMBL:Z14204; NID:g30967; PIND:CAA76573.1; PID:g309666  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotrimer; immunogloblin  
F/34-117/Domain: immunoglobulin homology <IM>  
  
Alignment Scores:  
Pred. No.: 2, 71e-43  
Score: 540.50  
Percent Similarity: 88.19%  
Best Local Similarity: 84.25%  
Query Match: 77.66%  
DB: 2  
  
Length: 139  
Matches: 107  
Conservative: 5  
Mismatches: 8  
Indels: 7  
Gaps: 2  
  
US-09-403-107-143\_COPY\_1\_381 (1-381) X S13674 (1-139)

Qy	1	GAAGTGCACCTCTGAGCTCGAGGGAGCGCTGGTCCAGCCTGGGAAGTCCCTGAGACTC	60
Db	20	GlnValGlnIleuValGlnIserGlyGlyIleValValGlnProGlyAAsgIserIleuArgIleu	39
Qy	61	TCCTGTGACGCTCTGATTCACCTTCAGTACGATAGGACATGCACTGGTCCGACAGCT	120
Db	40	SerCysAlaIleSerGlyPheThrPheSerSerIleArgIleThrIleStrValArgGlnAla	59
Qy	121	CCAGGCAAGGGGCTGGAGTGGGTGGCACTATATATCATATGATGGAGTAATAACTAT	180
Db	60	ProCysValGlyIleuGlnIleTrrValAlaValIleSerIleArgGlySerAlanIleIleTyr	79
Qy	181	GCAGATCTCGGTAAAGGGCGAATTCCATCTCCAGAGACAAATTCAGAAACAGCTGTAT	240
Db	80	AlaAspSerValIleGlyIleArgPheThrIleSerArgAspIleSerIleValAsnThrIleTyr	99
Qy	241	CTGCAATGAAACAGCTCTGAGACTGAGACACAGGCTGTGATTACTGTGCAAAATATG	300
Db	100	IleGlnIleMetAsnIserIleuArgAlaGlnAspIhrAlaValIleTyrIleCysAlaIleIys--Ala	118
Qy	301	GGGTGGGGCAGTGGCTGAGAACCTTACTTACTTACGATATGACGCTCTGGGCCAAGGG	360
Db	119	GlyIleuGlyIle-----PhePheAsnIrrPheAspProIrrGlyGlnGly	132
Qy	361	ACCAAGGTCAACGCTCTCTCTCA	381
Db	133	ThrIleuValThrValIleSerIle	139

Search completed: August 29, 2005, 11:31:16  
Job time : 19.0962 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 29, 2005, 11:01:36 ; Search time 81.1389 Seconds

(without alignments)  
4809.091 Million cell updates/sec

Title: US-09-403-107-143\_COPY\_1\_381

Perfect score: 696

Sequence: 1 gaggtgcagctgcgcgagctc.....ccacgctcacgcgtctctccca 381

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p\_model -DEV=xip  
-Q=/cgn2\_1/USPRO\_epool\_p/US09403107/runat\_29082005\_120124\_18889/app\_query.fasta\_1.1038  
-DB=uniprot -QEXT=faetan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09403107@cgn\_1\_1\_305@runat\_29082005\_120124\_18889 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESOURCE -NEG SCORES=0 -WAIT -DSPBLLOC=100 -LONGLOG  
-DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELXT=7

Database :  
1: uniprot\_03: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565.5	81.2	613	2 Q8WUK1	Q8WUK1 homo sapien
2	548	78.7	240	2 Q65ZC9	Q65ZC9 homo sapien
3	537	77.2	113	2 Q9UL90	Q9UL90 homo sapien
4	537	77.2	116	2 Q9UL93	Q9UL93 homo sapien
5	531	76.3	472	2 Q6N089	Q6N089 homo sapien
6	527.5	75.8	572	2 Q8WU38	Q8WU38 homo sapien
7	521.5	74.9	122	1 Q9Y509	Q9Y509 homo sapien
8	517.5	74.4	147	2 Q6P181	Q6P181 homo sapien
9	517	74.3	470	2 Q6P181	Q6P181 homo sapien
10	501	72.0	470	2 Q6P181	Q6P181 homo sapien
11	500.5	71.9	606	2 Q6GMY2	Q6GMY2 homo sapien
12	500	71.8	464	2 Q6WZU6	Q6WZU6 homo sapien
13	498.5	71.6	122	2 Q9UL84	Q9UL84 homo sapien
14	496.5	71.3	544	2 Q6P195	Q6P195 homo sapien
15	493	70.8	597	2 Q96B89	Q96B89 homo sapien
16	490	70.4	121	2 Q9UL71	Q9UL71 homo sapien

17	485.5	69.8	136	1 HV16	MOUSE	P01783	mus musculus
18	482	69.3	121	1 HV3J	HUMAN	P01771	homo sapien
19	479.5	68.9	126	1 HV3K	HUMAN	P01772	homo sapien
20	478.5	68.8	122	1 HV3H	HUMAN	P01769	homo sapien
21	473.5	68.0	473	2 Q6MZV7		Q6MZV7	homo sapien
22	470	67.5	493	2 Q6GMX2		Q6GMX2	homo sapien
23	467.5	67.2	116	1 HV3T	HUMAN	P01781	homo sapien
24	467	67.1	119	1 HV3T	HUMAN	P01770	homo sapien
25	465.5	66.9	118	2 Q9UL51		Q9UL51	homo sapien
26	463	66.5	499	2 Q8N5K4		Q8N5K4	homo sapien
27	462.5	66.5	487	2 Q6ZVX0		Q6ZVX0	homo sapien
28	462	66.4	493	2 Q8NCL6		Q8NCL6	homo sapien
29	461.5	66.3	475	2 Q6MZ06		Q6MZ06	homo sapien
30	461.5	66.3	487	2 Q99KX4		Q99KX4	mus musculus
31	460.5	66.2	479	2 Q6MZV6		Q6MZV6	homo sapien
32	458.5	65.9	475	2 Q6GMW7		Q6GMW7	homo sapien
33	457.5	65.7	473	2 Q91205		Q91205	mus musculus
34	456	65.5	485	2 Q6PDB8		Q6PDB8	mus musculus
35	456	65.5	519	2 Q6N092		Q6N092	homo sapien
36	455.5	65.4	118	2 Q9UL72		Q9UL72	homo sapien
37	455	65.4	482	2 Q7Z351		Q7Z351	homo sapien
38	454	65.2	120	1 HV3E	HUMAN	P01766	homo sapien
39	453.5	65.2	465	2 Q6P6C4		Q6P6C4	homo sapien
40	453.5	65.2	494	2 Q96K68		Q96K68	homo sapien
41	452	64.9	466	2 Q6IN78		Q6IN78	homo sapien
42	451.5	64.9	112	2 Q9HCC1		Q9HCC1	homo sapien
43	450	64.7	117	1 HV3C	HUMAN	P01764	homo sapien
44	450	64.7	493	2 Q68CN4		Q68CN4	homo sapien
45	448.5	64.4	120	1 HV3U	HUMAN	P01782	homo sapien

#### ALIGNMENTS

RESULT 1  
Q8WUK1 ID Q8WUK1 PRELIMINARY; PRT; 613 AA.  
AC Q8WUK1;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OC NCBI\_TaxID=9606;  
CX [1]  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Kryzhanovskiy M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.];  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC020240; AAH20240.1; -  
DR PIR: F36005; F36005.  
DR PIR: G36005; G36005.  
DR PIR: PH1642; PH1642.  
DR PIR: PH1643; PH1643.  
DR PIR: PH1645; PH1645.  
DR PIR: PH1646; PH1646.  
DR PIR: PLO098; PLO098.  
DR PIR: PLO120; PLO120.  
DR PIR: S15590; S15590.  
DR PIR: S31116; S31116.  
DR PIR: S31119; S31119.  
DR PIR: S70442; S70442.  
DR HSSP: P01861; 1ADQ.  
DR Pfam: PF07654; C1-set; 4.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PSS0835; IG LIKE; 5.  
DR PROSITE: PS00290; IG MHC; UNKNOWN; 3.  
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671B315 CRC64;  
  
Alignment Scores:  
Pred. No.: 4,09e-49 Length: 613  
Score: 565.50 Matches: 109  
Percent Similarity: 89.76% Conservative: 5  
Best Local Similarity: 85.83% Mismatches: 6  
Query Match: 81.25% Indels: 7  
DB: 2 Gaps: 2  
  
US-09-403-107-143\_COPY\_1\_381 (1-381) x 08WUK1 (1-613)  
QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGTCACAGCTGGAGAGTCCCTGAGACTC 60  
Db 20 GlnValGlnLeuValGlnSerGlyGlyValValGlnProGlyArgSerLeuArgLeu 39  
QY 61 TCCTGTGACAGCTCTGAGATTACCTTCAGTAGCTATGAGCATGAGTGGTCCGCGAGCT 120  
Db 40 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 59  
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGGATATATCATATGATGAAAGTAATAACTAT 180  
Db 60 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspIleSerAsnLysTyrTyr 79  
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATCCAGAAACAGCTGTAT 240  
Db 80 AlaAspSerValLysGlyArgPheThrIleSerThrGAspAsnSerLysAsnThrLeuTyr 99  
QY 241 CTGCAATGAACAGCGCTGAGAGCTGAGACACGCGTGTATTACTGTGCGAAAGATATG 300  
Db 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAsp--- 118  
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTACTAGGTATGACGCTCTGGGGCCAAAGG 360  
Db 119 ---TrrpSerGlnGlyValGlnTrpPhe-----AspIleTrpGlyGlnGly 132  
QY 361 ACCAGCGTACCGTCTCTCA 381  
Db 133 ThrMetValThrValSerSer 139  
  
RESULT 2  
Q65ZC9 PRELIMINARY; PRT; 240 AA.  
AC Q65ZC9;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Single-chain Fv (Fragment).  
GN Name=scFv;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=C1G/7;  
RX MEDLINE=97362799; PubMed=9219263;  
RA Kontermann R.E., Wing M.G., Winter G.;  
RT "Complement recruitment using bispecific diabodies";  
RL Nat. Biotechnol. 15:629-631(1997).  
DR EMBL: Y13056; CAA73499.1; -  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00409; Ig; 2.  
DR SMART: SM00406; IGV; 2.  
DR PROSITE: PSS0835; IG LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 240  
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;  
  
Alignment Scores:  
Pred. No.: 2,21e-47 Length: 240  
Score: 548.00 Matches: 106  
Percent Similarity: 88.19% Conservative: 6  
Best Local Similarity: 83.46% Mismatches: 5  
Query Match: 78.74% Indels: 10  
DB: 2 Gaps: 2  
  
US-09-403-107-143\_COPY\_1\_381 (1-381) x Q65ZC9 (1-240)  
QY 1 GAGGTGACAGCTGCTGAGTCTGGGGAGGCGCTGTCACAGCTGGAGAGTCCCTGAGACTC 60  
Db 1 GlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyArgSerLeuArgLeu 20  
QY 61 TCCTGTGACAGCTCTGAGATTACCTTCAGTAGCTATGAGCATGAGTGGTCCGCGAGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40  
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGGAGGATATATCATATGATGAAAGTAATAACTAT 180  
Db 41 ProGlyLysGlyLeuGlnTrpValAlaValIleSerTyrAspGlySerAsnLysTyrTyr 60  
QY 181 GCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATCCAGAAACAGCTGTAT 240  
Db 61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80  
QY 241 CTGCAATGAACAGCGCTGAGAGCTGAGACACGCGTGTATTACTGTGCGAAAGATATG 300  
Db 81 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyrTyrCysAlaLysAsp--- 99  
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTACTAGGTATGACGCTCTGGGGCCAAAGG 360  
Db 100 ---TrrpGlyAsp-----SerLeuAspProTrpGlyLysGly 110  
QY 361 ACCAGCGTACCGTCTCTCA 381  
Db 111 ThrLeuValThrValSerSer 117  
  
RESULT 3  
Q9UDJ90 PRELIMINARY; PRT; 113 AA.  
ID Q9UDJ90;  
AC Q9UDJ90;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 16, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;  
RW Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035024; AAD56260.1; -.  
DR PIR; S78486; S78486.  
DR HSSP; P01772; 2PB4.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT TER 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Alignment Scores:  
Pred. No.: 2.64e-46 Length: 113  
Score: 537.00 Matches: 104  
Percent Similarity: 85.04% Conservative: 4  
Best Local Similarity: 81.89% Mismatches: 5  
Query Match: 77.16% Indels: 14  
DB: 2 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x Q9UL90 (1-113)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGGAGGCGCTGTCAGGAGGTCCTGAGACTC 60  
DB 1 G|U|V|A|G|I|n|L|e|u|V|a|G|I|S|e|r|G|Y|G|I|V|A|G|I|n|P|r|o|G|I|S|e|r|L|e|u| 20  
QY 61 TCTGTGACGCTCTGATTCACCTTCAGTAGCTATGAGCATGACATGGGCTCGGAGGCT 120  
DB 21 S|e|r|C|y|S|a|I|a|S|e|r|G|Y|P|h|e|r|h|e|r|S|e|r|T|Y|G|Y|S|e|r|L|e|u| 40  
QY 121 CCAAGCAAGGGGCTGAGTGGTGGCAGTATATATATATATATATATATATATATATAT 180  
DB 41 P|r|o|G|I|S|e|r|L|e|u|G|I|n|T|P|V|A|I|A|V|A|I|L|e|r|T|Y|S|e|r|L|e|u| 60  
QY 181 GCAAGCTCCGTAAGGCGGAGTTCACATTCCTCCAGAGCAATTCAGAGAGGCTGAT 240  
DB 61 A|A|S|e|r|V|a|I|S|e|r|G|Y|A|S|e|r|T|Y|S|e|r|L|e|u| 80  
QY 241 CTGCAATGAACAGGCTGAGAGTGAAGACAGGCTGTGATTAATGCGAAGATATG 300  
DB 81 L|e|u|G|I|n|T|e|r|S|e|r|L|e|u|A|G|I|A|S|P|h|A|I|V|A|I|L|e|r|T|Y|C|y|S|a|I|a|Y|A|S|P|h|e|u| 100  
QY 301 GGGTGGGAGTGGCTGAGACCTTACTACTAGATGAGCTGGGGCCAGGG 360  
DB 101 A|e|r|T|Y|S|e|r|L|e|u|G|I|n|T|P|V|A|I|A|V|A|I|L|e|r|T|Y|S|e|r|L|e|u| 106  
QY 361 ACCACGTCACCTGCTCTCA 381  
DB 107 T|h|r|e|u|V|a|I|n|T|V|a|I|S|e|r|S|e|r| 113

## RESULT 4

Q9UL93 PRELIMINARY; PRT; 116 AA.  
AC Q9UL93.  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Young D.C.;  
RA Young X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035021; AAD56257.1; -.  
DR PIR; PH1644; PH1644.  
DR PIR; PLO120; PLO120.  
DR HSSP; P01772; 2PB4.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT TER 116  
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Alignment Scores:  
Pred. No.: 2.65e-46 Length: 116  
Score: 537.00 Matches: 105  
Percent Similarity: 86.51% Conservative: 7  
Best Local Similarity: 83.33% Mismatches: 10  
Query Match: 77.16% Indels: 10  
DB: 2 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x Q9UL93 (1-116)

QY 4 GTGACGCTGCTGAGTCTGGGGGAGGCGCTGTCAGGAGGTCCTGAGACTCTCC 63  
DB 1 V|a|G|I|n|L|e|u|V|a|G|I|S|e|r|G|Y|G|I|V|A|G|I|n|P|r|o|G|I|S|e|r|L|e|u| 20  
QY 64 TGTGACGCTCTGATTCACCTTCAGTAGCTATGAGCATGACATGGGCTCGGAGGCTTCA 123  
DB 21 C|y|S|a|I|a|S|e|r|G|Y|P|h|e|r|h|e|r|S|e|r|T|Y|G|Y|S|e|r|L|e|u| 40  
QY 124 GCGAAGGCGCTGAGTGGTGGCAGTATATATATATATATATATATATATATATAT 183  
DB 41 G|Y|S|e|r|L|e|u|G|I|n|T|P|V|A|I|A|V|A|I|L|e|r|T|Y|S|e|r|L|e|u| 60  
QY 184 GACCTCCGTAAGGCGGAGTTCACCATCTCCAGAGCAATTCAGAGAGGCTGATCTG 243  
DB 61 A|S|e|r|V|a|I|S|e|r|G|Y|A|S|e|r|T|Y|S|e|r|L|e|u| 80  
QY 244 CAAATGAACAGGCTGAGAGTGAAGACAGGCTGTGATTAATGCGAAGATATG 303  
DB 81 G|I|n|T|e|r|S|e|r|L|e|u|A|G|I|A|S|P|h|A|I|V|A|I|L|e|r|T|Y|C|y|S|a|I|a|Y|A|S|P|h|e|u| 100  
QY 304 TGGGGCAGTGGCTGGAACCTTACTACTACTACTACTACTACTACTACTACTACTACT 363  
DB 101 L|e|u|G|I|n|T|P|V|A|I|A|V|A|I|L|e|r|T|Y|S|e|r|L|e|u| 110  
QY 364 ACGTCAACGCTCTCTCA 381  
DB 111 L|e|u|V|a|I|n|T|V|a|I|S|e|r|S|e|r| 116

## RESULT 5

Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686P15220.  
GN Name=DKFZp686P15220.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wandut R., Heudner D., Nemes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640627; CAB45781.1; -.  
DR HSSP; P01861; 1ADQ.

DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG\_C1.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_Y.  
DR Pfam: PF07654; C1-set; 3.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IG; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS50835; IG LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D046D279 CRC64;

Alignment Scores:  
Pred. No.: 1,37e-45 Length: 472  
Score: 531.00 Matches: 101  
Percent Similarity: 88.19% Conservative: 11  
Best Local Similarity: 79.53% Mismatches: 11  
Query Match: 76.29% Indels: 4  
DB: 2 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x Q6N089 (1-472)

QY 1 GAGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGATCCAGCGCTGGAGTCCCTGAGACTC 60  
DB 20 GIVVAGLIneuValGluSerGlyGlyGlyLeuValGlnProGlyArgSerLeuAlaGlu 39  
QY 61 TCGTGTGAGCGCTCTGGATTACCTTCAGTAGCTATGAGCAGTGGTCCGCAAGGCT 120  
DB 40 SerCyAlaAlaSerGlyPheThrPheAspPtyrAlaMetHisTrpValArgGlnAla 59  
QY 121 CCAGGCAAGGGCTGGAGTGGGTGGGAGCTATATCATATGATAGTAATAATCTAT 180  
DB 60 ProGlyLysGlyLeuGluTrpValSerGlyIleSerTrpAsnSerGlyLeuAlaTyr 79  
QY 181 GCAGACTCCGCTGAAGGGCCGATTCAACCATCTCCAGAGCAATTCAGAACACGCTGTAT 240  
DB 80 AlaAspSerValLysGlyArgPheThrIleSerArgAspSerGlyLysAsnSerLeuTyr 99  
QY 241 CTCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTACTGTGCGAATATGAT 300  
DB 100 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrCysAlaLysGlnIle 119  
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTAGGTATGAGCGTGGGCGCAAGG 360  
DB 120 GYAlaHisAsn-----PheTyrTyrTyrTyrMetAspValTrpGlyGlnGly 135  
QY 361 ACCACGGTCACCGTCTCTCA 381  
DB 136 ThrThrValThrValSerSer 142

RESULT 6

Q8WU38 PRELIMINARY; PRT; 573 AA.

ID Q8WU38  
AC Q8WU38; MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Primary B-Cells;  
MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,  
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
RA Villalón D.K., Muzny D.C., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Maira M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC021276; AAH21276.1; --  
DR PIR: S21205; S21205.  
DR PIR: S30532; S30532.  
DR HSSP: P18529; 118K.  
DR Pfam: PF07654; C1-set; 2.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS50835; IG LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Alignment Scores:  
Pred. No.: 3,24e-45 Length: 573  
Score: 527.50 Matches: 103  
Percent Similarity: 87.40% Conservative: 8  
Best Local Similarity: 81.10% Mismatches: 13  
Query Match: 75.79% Indels: 3  
DB: 2 Gaps: 1

US-09-403-107-143\_COPY\_1\_381 (1-381) x Q8WU38 (1-573)

QY 1 GAGGTGAGCTGCTCGAGTCTGGGGAGGCGCTGATCCAGCGCTGGAGTCCCTGAGACTC 60  
DB 20 GIVVAGLIneuValGluSerGlyGlyGlyLeuValGlnProGlyArgSerLeuAlaGlu 39  
QY 61 TCGTGTGAGCGCTCTGGATTACCTTCAGTAGCTATGAGCAGTGGTCCGCAAGGCT 120  
DB 40 SerCyAlaAlaSerGlyPheThrPheAspPtyrAlaMetHisTrpValArgGlnAla 59  
QY 121 CCAGGCAAGGGCTGGAGTGGGTGGGAGCTATATCATATGATAGTAATAATCTAT 180  
DB 60 ProGlyLysGlyLeuGluTrpValSerGlyIleSerTrpAsnSerGlyLeuAlaTyr 79  
QY 181 GCAGACTCCGCTGAAGGGCCGATTCAACCATCTCCAGAGCAATTCAGAACACGCTGTAT 240  
DB 80 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyr 99  
QY 241 CTCGAATGAACAGCTGAGAGCTGAGAGACAGGCTGTATTACTGTGCGAATATGAT 300  
DB 100 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrCysAlaLysGlnIle 118  
QY 301 GGGTGGGCGAGTGGCTGAGAACCTTACTACTAGGTATGAGCGTGGGCGCAAGG 360  
DB 119 -----GlySerGlySerTyrIleGlyTyrTyrTyrMetAspValTrpGlyGlnGly 136

RESULT 7

HV3G\_HUMAN STANDARD; PRT; 122 AA.

ID HV3G\_HUMAN  
AC HV3G\_HUMAN; MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Primary B-Cells;  
MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

```
AC P01768;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MICELANOUS; This mu chain was isolated from the plasma of a
CC patient with macroglobulinemia.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02051; M3HUM.
DR HSBP; P01772; 2P84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00447; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252P1C2 CRC64;

Alignment Scores:
Pred. No.: 1,05e-44 Length: 122
Score: 521.50 Matches: 97
Percent Similarity: 86.05% Conservative: 14
Best Local Similarity: 75.19% Mismatches: 9
Query Match: 74.93% Indels: 9
DB: 1 Gaps: 2

US-09-403-107-143_COPY_1_381 (1-381) x HV3G_HUMAN (1-122)
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
DB 1 GlnValGlnLeuValGlnSerGlyGlyValVal****ProGlyArgSerLeuArgLeu 20
QY 61 TCCGTGACGCTGCTGAGTTCACCTTCAGTAGCTATGCGATGCACTGGGTCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrlaMetHleTrrValArgGlnPro 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCACTTATATCATATGATGAAGTAATAAATACAT 180
DB 41 ProGlyLysGlyLeuAlaTrrPalaAlaValIleSerTyr****Gly****LysTrrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCCATCTCCAGAGACAATTCAGAGACACGCTGAT 240
DB 61 Ala****SerValLysGlyArgPheThrIleSerArgAsp****SerLys****ThrLeuTyr 80
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGACACGCGCTGTGATTAATGTCGAAAGATATG 300
DB 81 LeuGlnMetAsnSerLeuArgAlaGlu****ThrAlaValTrrTyrCysAlaArgAsp--- 99
QY 301 GGGTGGGGCAGTGGCTGAGACCCCTACAC-----TACTACGGATATGAGAGTCTGGGGC 354
DB 100 -----ArgProLeuTrrGly****TrrArgAlaAlaPheAsnTrrTrrPgly 113
QY 355 CAAGGACACAGGTCACCGTCTCTCTCA 381
DB 114 GlnGlyThrLeuValThrValSerSer 122
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RESULT 8
QY509 PRELIMINARY; PRT; 147 AA.
AC QY509;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE VH3 protein (Fragment).
GN Name=VH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=745228;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers."
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSBP; P01842; 1AOK.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Alignment Scores:
Pred. No.: 2.78e-44 Length: 147
Score: 517.50 Matches: 99
Percent Similarity: 85.83% Conservative: 10
Best Local Similarity: 77.95% Mismatches: 17
Query Match: 74.35% Indels: 1
DB: 2 Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x QY509 (1-147)
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTCACGCTGGAGGTCCTGAGACTC 60
DB 1 GlnValHsleuValGlnSerGlyGlyValValGlnProGlyLysSerLeuArgLeu 20
QY 61 TCCGTGACGCTGCTGAGTTCACCTTCAGTAGCTATGCGATGCACTGGGTCGCCAGGCT 120
DB 21 SerCysGlnAlaSerGlyPheThrPheSerThrTrrGlyMetSerTrrPalaArgGlnAla 40
QY 121 CCAGGCAAGGGGCTGAGTGGGTGGCACTTATATCATATGATGAAGTAATAAATACAT 180
DB 41 ProGlyLysGlyLeuAspTrrPalaAlaLeuIleSerTrrAspGlySerThrGlnTrrTyr 60
QY 181 GCAGACTCCGTGAAGGGCCGATTCCATCTCCAGAGACAATTCAGAGACACGCTGAT 240
DB 61 AlaGlySerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80
QY 241 CTGCAATGAACAGCCTGAGAGCTGAGACACGCGCTGTGATTAATGTCGAAAGATATG 300
DB 81 LeuGlnMetThrSerLeuArgValGlnAspTrrAlaValTrrTyrCysAlaLysAspGly 100
QY 301 GGGTGGGGCAGTGGCTGAGACCCCTACTACTACTACGATGAGACGCTGGGGCCAGAGG 360
DB 101 AsnTrrPheAspSer---ValGlyTrrTrrTrrAlaGlyLleAspTrrTrrPglyGlnGly 119
QY 361 ACAAGGTCACCGTCTCTCTCA 381
DB 120 ThrLeuValThrValSerSer 126

RESULT 9
Q6P181
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ID 06P181 PRELIMINARY; PRT; 478 AA.
AC 06P181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sec; 3.
DR SMART; SM00409; IGC1; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ
SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Alignment Scores:
Pred. No. 3.77e-44 Length: 478
Score: 517.00 Matches: 102
Percent Similarity: 85.27% Conservative: 8
Best Local Similarity: 79.07% Mismatches: 17
Query Match: 74.28% Indels: 2
DB: Gaps: 1

US-09-403-107-143_COPY_1_381 (1-381) x 06P181 (1-478)
QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGTGTCACGCTGGAGCTCCCTGAGATC 60
DB 20 G1uValG1nleuValG1uSerG1yG1yG1eValG1nProG1ySerLeuArgLeu 39
QY 61 TCCCTGACAGCTCTGATTCACCTTCAGAGCAGATGACATGCATGGGTCCGACAGCT 120
DB 40 SerGyAlaAlaSerG1yPheThrPheSerSerTyrrPheMetSerTyrrValArgGlnAla 59

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QY 121 CCAGGCAAGGCGCTGAGTGGGTGACAGTTATATCATATGATGAGATTAATAATAT 180
DB 60 ProG1ySerG1yLeuG1uTrpValAlaSerLeuG1yGlnAseP1ySerLyuSerTyrrTy 79
QY 181 GCAAGACTCCGTGAAGGCGCGATTCACCATCTCCAGAGACATTCAGAAACGCTGTAT 240
DB 80 ValAAsPserVallySerG1yArgPheThrIleSerArgAsPAsnAlaIyAsnSerLeuTy 99
QY 241 CTGCAAAATGACAGCTGAGAGCTGAGGACACAGGCGTGTATTAAGTGGTGAAGATATG 300
DB 100 LeuG1nMetAsnSerLeuArgAlaG1uAsP1nAlaValTyrrTyrrCyAlaArgG1uPne 119
QY 301 -----GGGTGGGCGAGTGGCTGAGACCCCTACTACTACGAGTATGACGCTGGGCG 354
DB 120 GluSerThrMetThrThrValAlaSerValAlaAsP1yTyrrTyrrPheTyMetAsPAlTrpG1y 139
QY 355 CAAGGACCAACGCTCACCGCTCTCTCA 381
DB 140 LysG1yThrThrValThrValSerSer 148

RESULT 10
Q6P181 PRELIMINARY; PRT; 470 AA.
ID 06P181;
AC 06P181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sec; 3.
DR SMART; SM00409; IGC1; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.

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DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein  
 SQ SEQUENCE 470 AA; 5175 MW; 7849556A11FD7D9 CRC64;

Alignment Scores:  
 Pred. No.: 1,666-42 Length: 470  
 Score: 501.00 Matches: 100  
 Percent Similarity: 81.89% Conservative: 4  
 Best Local Similarity: 78.74% Mismatches: 17  
 Query Match: 71.98% Indels: 6  
 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x O6GMV4 (1-470)

QY 1 GAGGTGAGCTGCTGAGTCTGGGAGAGCCCTGCTCAGCTGGAAGCTCCTGAGACTC 60  
 DB 20 GlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39  
 QY 61 TCCTGTGAGCTGCTGAGTTCACCTTACCTAGCTATGACGACGCTGGGCTCCGAGGCT 120  
 DB 40 SerCysValValSerGlyPheThrPheSerSerTyTrpMetSerTrpValArgGlnAla 59  
 QY 121 CCAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAGTAATATATATAT 180  
 DB 60 ProGlyGlyGlyLeuGlyLeuTrpValAlaAlaSerGlyGlySerGlyLeuTyTrp 79  
 QY 181 GCAGACTCTCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCAGAGAACACGCTGAT 240  
 DB 80 ValAspSerValValGlyArgPheThrIleSerArgAspAsnAlaValAsnSerLeuTy 99  
 QY 241 CTGCAAAAGAAACAGCTGAGCTGAGGACAGGCTGGTGTATCTATGCGCAAGATATNG 300  
 DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTrpCysAlaArgAsp 118  
 QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATGATGACGCTGGGCGCAAGG 360  
 DB 119 -----GlySerSerTrp-----TyrArgAspTrpPheAspProTrpGlyGlnGly 133  
 QY 361 ACCAGGCTACCCCTCTCTCTCA 381  
 DB 134 ThrLeuValThrValSerSer 140

RESULT 11  
 O6GMV2 PRELIMINARY; PRT; 606 AA.

AC O6GMV2  
 DT 05-JUL-2004 (TRENBLREL. 27, Created)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISU8-Primary B-Cells;  
 RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rane S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boeak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Kuzny D.W., Sodergren B.V., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISU8-Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073758; AAH73758.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 4.  
 DR Pfam; PF00047; IG; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Alignment Scores:  
 Pred. No.: 1,94e-42 Length: 606  
 Score: 500.50 Matches: 100  
 Percent Similarity: 79.56% Conservative: 9  
 Best Local Similarity: 72.99% Mismatches: 15  
 Query Match: 71.91% Indels: 13  
 Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x O6GMV2 (1-606)

QY 1 GAGGTGAGCTGCTGAGTCTGGGAGAGCCCTGCTCAGCTGGAAGCTCCTGAGACTC 60  
 DB 20 GlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39  
 QY 61 TCCTGTGAGCTGCTGAGTTCACCTTACCTAGCTATGACGACGCTGGGCTCCGAGGCT 120  
 DB 40 SerCysValValSerGlyPheThrPheSerSerTyTrpMetSerTrpValArgGlnAla 59  
 QY 121 CCAGGCAAGGGGCTGAGTGGTGGCAGTTATATCATATGATGAGTAATATATATAT 180  
 DB 60 ProGlyGlyGlyLeuGlyLeuTrpValAlaAlaSerGlyGlySerGlyLeuTyTrp 79  
 QY 181 GCAGACTCTCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCAGAGAACACGCTGAT 240  
 DB 80 ValAspSerValValGlyArgPheThrIleSerArgAspAsnAlaValAsnSerLeuTy 99  
 QY 241 CTGCAAAAGAAACAGCTGAGCTGAGGACAGGCTGGTGTATCTATGCGCAAGATATNG 300  
 DB 100 LeuGlnMetAsnSerLeuArgAlaGlnAspThrAlaValTyTrpCysAlaArgAsp 118  
 QY 301 GGGTGGGGCAGTGGCTGAGAGACCTTACTACTACGATGATGACGCTGGGCGCAAGG 360  
 DB 119 -----GlySerSerTrp-----TyrArgAspTrpPheAspProTrpGlyGlnGly 136  
 QY 361 TACTACGCTATGAGCTGCTGGGAGAGCCCTGCTCAGCTGGAAGCTCCTGAGACTC 381  
 DB 137 TyrTrpGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 153

RESULT 12  
 O6MZU6 PRELIMINARY; PRT; 464 AA.

AC O6MZU6  
 DT 05-JUL-2004 (TRENBLREL. 27, Created)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)  
 DE Hypothetical protein DKFP686C15213.  
 GN Name=DKFP686C15213;



OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Oesanger A.,  
RDO G., Han M., Wiemann S.,  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640874; CAE4531.1; -  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003596; Ig\_Mc.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-sec; 3.  
DR SMART; SM00409; Ig; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KM Hypothetical protein.  
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C6E8A0BC CRC64;

Alignment Scores:  
Pred. No.: 2,09e-42 Length: 464  
Score: 500.00 Matches: 97  
Percent Similarity: 85.16% Conservative: 12  
Best Local Similarity: 75.78% Mismatches: 9  
Query Match: 71.84% Indels: 10  
DB: Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x Q6MZD6 (1-464)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGGTCCAGGCTGGAGAGTCCCTGAGACTC 60  
DB 20 GtUvaIgHleuValIgUserGlyGlyValGleuValIysProGlyIysSerleuValGleu 39  
QY 61 TCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCCAGGCT 120  
DB 40 SerCysAlaIaIaSerGlyPheThrPheSerSerTySerMetCysAntrValArgGlnAla 59  
QY 121 CCAAGGCAAGGGGCTGGAGTGGGTGGGAGCTATA---TCATATGATGGAATTAATATAC 177  
DB 60 ProGlyIysGlyLeuGluTrpValSerSerPheSerSerArgGlyIysSerTyArgIuTy 79  
QY 178 TATGCAACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGACAGGCTG 237  
DB 80 TyrAlaAspSerValIysGlyArgPheThrIleSerArgAspAlaIysAsnMetCysLeu 99  
QY 238 TATTCGAAATGAACACGCTGAGAGCTGAGACACGCGCTGTGTATTACTGTGCGAAAGAT 297  
DB 100 TyrleuGlnMetAsnSerleuArgAlaGluAsnThrAlaValTyTyTyCysAlaArgAsp 119  
QY 298 ATGGGGTGGGGAGTGGCTGAGACCTACTACTACTACGATATGACGCTGTGGGGCGCA 357  
DB 120 leuGlyTrp-----PheGlyLeuAspTyTyTrpGlyGln 130  
QY 358 GGGACACGAGCTGACCGTCTCTCA 381  
DB 131 GlyThrleuValThrValSerSer 138

RESULT 13  
Q9UL84 PRELIMINARY; PRT; 122 AA.  
AC Q9UL84;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Meewe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus."  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL EMBL; AF035030; AAD56266.1; -  
DR HSSP; P01772; 2F84.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 122  
FT NON\_TER 1 122  
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Alignment Scores:  
Pred. No.: 2.41e-42 Length: 122  
Score: 498.50 Matches: 101  
Percent Similarity: 84.25% Conservative: 6  
Best Local Similarity: 79.53% Mismatches: 15  
Query Match: 71.62% Indels: 5  
DB: Gaps: 2

US-09-403-107-143\_COPY\_1\_381 (1-381) x Q9UL84 (1-122)

QY 1 GAGGTGACGCTGCTGAGTCTGGGGAGGCGCTGGTCCAGGCTGGAGAGTCCCTGAGACTC 60  
DB 1 GtUvaIgHleuValIgUserGlyGlyValGleuValIysProGlyIysSerleuValGleu 20  
QY 61 TCTGTGACGCTCTGTGATTCACCTTCAGTAGCTATGAGCATGCACTGGTCCGCCAGGCT 120  
DB 21 SerCysAlaIaIaSerGlyPheThrPheSerSerTySerMetCysAntrValArgGlnAla 40  
QY 121 CCAAGGCAAGGGGCTGGAGTGGGTGGGAGCTATAATCATATGATGAGAAATTAATCTAT 180  
DB 41 ProGlyIysGlyLeuGluTrpValAlaIaIaIleSerArgAspAsnSerTyAsnMetCysLeu 60  
QY 181 GCAAGACTCCGCTGAAGGGCCGATTCACCATCTCCAGAGCAATTCAGAGACAGGCTGAT 240  
DB 61 AlaAspSerValIysGlyArgPheThrIlePheArgAspAsnSerTyAsnMetCysLeu 80  
QY 241 CTGCAATATGAACAGCTGAGAGCTGAGACAGGCTGTGTATTACTGTGCGAAAGATATG 300  
DB 81 leuGlnMetAsnSerleuArgAlaGluAspThrAlaValTyTyTyCysAlaArgAsp---- 99  
QY 301 GGGTGGGGAGTGGCTGAGACCTACTACTACTACGATATGACGCTGTGGGGCGCAAGG 360  
DB 100 -----GluArgGlyArgleuValGlyThrTyPhe-----AspTyTrpGlyGlnGly 115  
QY 361 ACCAGGTGACCGTCTCTCA 381  
DB 116 ThrleuValThrValSerSer 122

RESULT 14  
Q6RP95 PRELIMINARY; PRT; 544 AA.  
AC Q6RP95;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;





US-09-403-107-143\_copy\_1\_381 (1-381) x Q96BB9 (1-597)

```

QY      1 GAGGTGAGCTGCTCGAGTCTGGGGAGAGCCTGGTCCAGCCTGGAGGCTCCCTGAGACTC 60
      |||||||
Db      20 GluValGlnLeuLeuGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
      |||||||
QY      61 TCCGTGTCAGCCTCTGGATTCACTTCAGTATGTCATGCACTGGGTCCGCCAGGCT 120
      |||||||
Db      40 SerCysAlaIleAspSerGlyPheSerPheSerTyrAlaMetValThrValArgGlnAla 59
      |||||||
QY      121 CCAAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGTAATAATACTAT 180
      |||||||
Db      60 ProGlyLysGlyLeuGlnuTTPValSerAlaIleSerGlySerGlySerThrTyrTyr 79
      |||||||
QY      181 GCAGACTCCCTGMAAGGCCGATTCAACCATCTCCAGAGACAAATCCAAAGAACAGCTGTAT 240
      |||||||
Db      80 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThrLeuTyr 99
      |||||||
QY      241 CTCCAATGAACAGCCTGAGAGCTGAGAGACACGGCTGTATTACTGTGCGAAAGAT--- 297
      |||||||
Db      100 LeuGlnMetAsnSerLeuAlaGlnAspThrAlaValTyrTyrCysAlaIysAspPro 119
      |||||||
QY      298 ATGGGGTGGGGCAGTGGCTGGAGACCTCTACTACTACTACGGTATGACGCTGGGGGCCAA 357
      |||:::
Db      120 ArgGlyTyrSerAlaSerGlyAsn-----TyrThrArgGlnAspTyrTrpGlyGln 136
      |||
QY      358 GGGACCAACGGTCAACCGTCTCTCTCA 381
      |||||
Db      137 GlyThrLeuValThrValSerSer 144

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Search completed: August 29, 2005, 11:06:48  
Job time : 84.1389 secs